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FILE 'HOME' ENTERED AT 13:07:27 ON 20 SEP 2005

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=> s (integrating plasmid)

L1 272 (INTEGRATING PLASMID)

=> s candida utilis

5634 CANDIDA UTILIS

=> s 12 and (biotin synthase)

11 L2 AND (BIOTIN SYNTHASE)

=> d 13 ti abs ibib tot

ANSWER 1 OF 11 USPATFULL on STN T.3

TIMethods for monitoring multiple gene expression

The present invention relates to methods for monitoring differential AB expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays containing filamentous fungal expressed sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates containing such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2005:140340 USPATFULL

Methods for monitoring multiple gene expression TITLE: INVENTOR(S): Berka, Randy M., Davis, CA, UNITED STATES

Rey, Michael W., Davis, CA, UNITED STATES Shuster, Jeffrey R., Davis, CA, UNITED STATES

Kauppinen, Sakari, Smoerum, DENMARK Clausen, Ib Groth, Hillerod, DENMARK Olsen, Peter Bjarke, Copenhagen, DENMARK

PATENT ASSIGNEE(S): Novozymes Biotech, Inc., Davis, CA, UNITED STATES (U.S.

corporation)

Novozymes A/S, Bagsvaerd, DENMARK (non-U.S.

corporation)

NUMBER KIND DATE -----US 6902887 B1 20050607 PATENT INFORMATION:

APPLICATION INFO.: US 2000-533559 20000322 (9) Continuation-in-part of Ser. No. US 1999-273623, filed RELATED APPLN. INFO.:

on 22 Mar 1999, ABANDONED

DOCUMENT TYPE: Utility GRANTED FILE SEGMENT:

PRIMARY EXAMINER: Brusca, John S. LEGAL REPRESENTATIVE: Stames, Robert L.

NUMBER OF CLAIMS: 8 EXEMPLARY CLAIM:

NUMBER OF DRAWINGS: 0 Drawing Figure(s); 0 Drawing Page(s)

LINE COUNT: 18386

#### CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 2 OF 11 USPATFULL on STN L3

ΤI Methods for monitoring multiple gene expression

AB The present invention relates to methods for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays containing filamentous fungal expressed sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates containing such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2004:292283 USPATFULL

TITLE:

Methods for monitoring multiple gene expression

INVENTOR(S):

Berka, Randy M., Davis, CA, UNITED STATES Rey, Michael W., Davis, CA, UNITED STATES Shuster, Jeffrey R., Davis, CA, UNITED STATES

Kauppinen, Sakari, Smoerum, DENMARK Clausen, Ib Groth, Hillerod, DENMARK Olsen, Peter Bjarke, Copenhagen, DENMARK

PATENT ASSIGNEE(S):

Novozymes Biotech, Inc., Davis, CA (U.S. corporation) Novozymes A/S, Inc., Bagsvaerd, DENMARK (U.S.

corporation)

	NUMBER	KIND	DATE
JS	2004229367	A1	20041118

PATENT INFORMATION: APPLICATION INFO.:

US 2003-653047

**A**1 20030829 (10)

RELATED APPLN. INFO.:

Division of Ser. No. US 2000-533559, filed on 22 Mar 2000, PENDING Continuation-in-part of Ser. No. US

1999-273623, filed on 22 Mar 1999, ABANDONED

DOCUMENT TYPE: FILE SEGMENT:

Utility APPLICATION

LEGAL REPRESENTATIVE:

NOVOZYMES BIOTECH, INC., 1445 DREW AVE, DAVIS, CA,

95616

NUMBER OF CLAIMS:

EXEMPLARY CLAIM:

Я 1

LINE COUNT:

19697

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 3 OF 11 USPATFULL on STN L3

ΤI Yeast with high biotin-productivity and the preparation method thereof AΒ The invention discloses a yeast with high biotin-productivity and the preparation method thereof. The yeast is transformed by an integrated plasmid, which includes a biotin synthase gene, an assistant DNA sequence for the integration of the plasmid into a host

genome, a promoter sequence, and a selection marker.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2003:152918 USPATFULL

TITLE:

Yeast with high biotin-productivity and the preparation

method thereof

INVENTOR(S):

Shiuan, David, Kaohsiung, TAIWAN, PROVINCE OF CHINA

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003104584	A1	20030605	(9)
APPLICATION INFO.:	US 2001-752957	A1	20010102	

NUMBER DATE PRIORITY INFORMATION: TW 2000-89120972 20001007

DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION

BRUCE LONDA, NORRIS, MCLAUGHLIN & MARCUS, P.A., 220 LEGAL REPRESENTATIVE:

EAST 42ND STREET, 30TH FLOOR, NEW YORK, NY, 10017

NUMBER OF CLAIMS: EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 13 Drawing Page(s)

LINE COUNT: 486

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 4 OF 11 USPATFULL on STN L3

ΤI Novel Polynucleotides

AB Novel polynucleotides derived from microorganisms belonging to coryneform bacteria and fragments thereof, polypeptides encoded by the polynucleotides and fragments thereof, polynucleotide arrays comprising the polynucleotides and fragments thereof, recording media in which the nucleotide sequences of the polynucleotide and fragments thereof have been recorded which are readable in a computer, and use of them.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2002:343879 USPATFULL Novel Polynucleotides

TITLE: INVENTOR(S):

Nakagawa, Satoshi, Tokyo, JAPAN

Mizoguchi, Hiroshi, Tokyo, JAPAN

Ando, Seiko, Tokyo, JAPAN Hayashi, Mikiro, Tokyo, JAPAN Ochiai, Keiko, Tokyo, JAPAN Yokoi, Haruhiko, Tokyo, JAPAN Tateishi, Naoko, Tokyo, JAPAN Senoh, Akihiro, Tokyo, JAPAN Ikeda, Masato, Tokyo, JAPAN Ozaki, Akio, Hofu-shi, JAPAN

	NUMBER	KIND	DATE	
US	2002197605	A1	20021226	
IIC	2000-738626	Δ1	20001219	101

PATENT INFORMATION: APPLICATION INFO.:

US 2000-738626 20001218

		NUMBER	DATE
PRIORITY	INFORMATION:	JP 1999-377484	19991216
		JP 2000-159162	20000407
		JP 2000-280988	20000803
DOCUMENT	TYPE:	Utility	

DOCUMENT TYPE:

FILE SEGMENT: APPLICATION LEGAL REPRESENTATIVE:

NIXON & VANDERHYE P.C., 8th Floor, 1100 North Glebe

Road, Arlington, VA, 22201

NUMBER OF CLAIMS: 68 EXEMPLARY CLAIM:

1

NUMBER OF DRAWINGS:

4 Drawing Page(s)

LINE COUNT:

13673

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 5 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN L3

ΤI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

ΑN DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09589 DNA DGENE

New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

(SHIU-I)SHIUAN D. PATENT ASSIGNEE:

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: PCR primer #1 for S. cerevisiae BIO2 gene.

L3 ANSWER 6 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN

New integrated plasmid, useful for preparing yeast with high biotin-TIproductivity used as feed additives, food additives or cosmetics.

AN ADA09591 DNA DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a degenerate PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09591 DNA

DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 TW 2000-120972 PRIORITY INFO: 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: Degenerate PCR primer #1 for C. utilis BIO2 gene.

ANSWER 7 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN 1.3

ΤI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09590 DNA **DGENE** 

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09590 DNA **DGENE** 

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

PCR primer #2 for S. cerevisiae BIO2 gene. DESCRIPTION:

ANSWER 8 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN .L3

ΤI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09592 DNA DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a

degenerate PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09592 DNA DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

Shiuan D INVENTOR:

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

20 PATENT INFO: US 2003104584 A1 20030605

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: Degenerate PCR primer #2 for C. utilis BIO2 gene.

ANSWER 9 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN L3

New integrated plasmid, useful for preparing yeast with high biotin-ΤI productivity used as feed additives, food additives or cosmetics.

AN ADA09588 DNA DGENE

The present invention relates to a yeast with high biotin-productivity AB and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents C. utilis

biotin synthase gene.

ACCESSION NUMBER: ADA09588 DNA DGENE

New integrated plasmid, useful for preparing yeast with high TITLE:

biotin- productivity used as feed additives, food additives

or cosmetics.

Shiuan D INVENTOR:

PATENT ASSIGNEE: (SHIU-I)SHIUAN D.

20 PATENT INFO: US 2003104584 A1 20030605

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent English LANGUAGE:

OTHER SOURCE: 2003-567956 [53] Candida utilis biotin DESCRIPTION:

#### synthase gene.

ANSWER 10 OF 11 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN L3

New integrated plasmid, useful for preparing yeast with high TT biotin-productivity used as feed additives, food additives or cosmetics.

AN 2003-567956 [53] WPIDS

AB US2003104584 A UPAB: 20030820

> NOVELTY - An integrated plasmid comprising a biotin synthase gene, an assistant DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

- (1) a method for preparing a yeast with high biotin-productivity comprising constructing the integrated plasmid cited above, linearizing the integrated plasmid, transforming the linearized integrated plasmid into a yeast, and recombining the biotin synthase gene with the yeast genome; and
- (2) a method for producing biotin comprising providing the yeast with high biotin-productivity, culturing the yeast in a nutrient medium, and recovering biotin from the culture broth.

USE - The integrated plasmid is useful for preparing yeast with high biotin-productivity. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics (all claimed).

Dwq.0/13

ACCESSION NUMBER:

2003-567956 [53] WPIDS

DOC. NO. CPI:

C2003-153236

TITLE:

New integrated plasmid, useful for preparing yeast with

high biotin-productivity used as feed additives, food

additives or cosmetics.

DERWENT CLASS:

C06 D13 D16 D21

INVENTOR(S):

SHIUAN, D

PATENT ASSIGNEE(S):

(NASC-N) NAT SCI COUNCIL; (SHIU-I) SHIUAN D

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO	KIND DATE	WEEK	LA PG
US 2003104584 TW 220675	A1 20030605 B1 20040901		20

#### APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2003104584	A1	US 2001-752957	20010102
TW 220675	B1	TW 2000-120972	

PRIORITY APPLN. INFO: TW 2000-120972 20001007

L3 ANSWER 11 OF 11 BIOTECHDS COPYRIGHT 2005 THE THOMSON CORP. on STN ΤI New integrated plasmid, useful for preparing yeast with high

biotin-productivity used as feed additives, food additives or cosmetics: vector-mediated gene transfer and expression in host cell for strain improvement and feed additive, food additive or cosmetic manufacture

ΑN 2003-20688 BIOTECHDS

AB DERWENT ABSTRACT:

> NOVELTY - An integrated plasmid comprising a biotin synthase gene, an assistant DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) a method for preparing a yeast with high biotin-productivity comprising constructing the integrated plasmid cited above, linearizing the integrated plasmid, transforming the linearized integrated plasmid into a yeast, and recombining the biotin synthase gene with the yeast genome; and (2) a method for producing biotin comprising providing the yeast with high biotin-productivity, culturing the yeast in a nutrient medium, and recovering biotin from the culture broth.

BIOTECHNOLOGY - Preferred Plasmid: The biotin synthase gene of the integrated plasmid is derived from Saccharomyces cerevisiae or Candida utilis. The biotin synthase gene of C. utilis comprises a fully defined sequence of 1188 base pairs (bp) given in the specification. The assistant DNA sequence is a C. utilis fragment consisting of NsiI-BamHI 18s rDNA, URA3 DNA, or HIS3 DNA. The selection marker is preferably a cycloheximide-resistant gene. The promoter sequence is pL41 promoter of C. utilis or pADH1 promoter of S. cerevisiae. The integrated plasmid is: (A) pMCC21 comprising pL41 for the expression of C. utilis BIO2 gene encoding for 204 amino acids, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis 18S rDNA; (B) pMCC31S or pMCC38S comprising pL41 for the expression of C. utilis BIO2 gene encoding for 233 amino acids, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis 18S rDNA; (C) pMCC32H or pMCC36H comprising C. utilis pL41, C. utilis BIO2 gene, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis HIS3 gene fragment; or (D) pMCC33U or pMCC35U comprising C. utilis pL41, C. utilis BIO2 gene, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis URA3 gene fragment.

USE - The integrated plasmid is useful for preparing yeast with high biotin-productivity. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics (all claimed).

EXAMPLE - Polymerase chain reaction (PCR) was carried out using the Candida utilis BIO2 gene as a template. The product was digested with NdeI and SalI, and ligated into pMC5 to obtain pMCC11. The NdeI-SalI fragment of pMCC11 in which the NdeI nickel was end-repaired into a blunt end by Klenow DNA polymerase (i.e. pL41-BIO2 fragment) was ligated into pMC9 to obtain pMCC15. To fill the lost L41 fragment, the BamHI-EcoRI fragment of pMC9 (i.e. L41 gene fragment) was end-repaired into a blunt end by Klenow DNA polymerase and then integrated into the SalI site in pMCC15 to obtain pMCC21. The plasmid pMCC21 comprises C. utilis pL41 for the expression of the C. utilis BIO2 gene, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis 18S rDNA. (20 pages)

ACCESSION NUMBER: 2003-20688 BIOTECHDS

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin-productivity used as feed additives, food additives or.

cosmetics;

vector-mediated gene transfer and expression in host cell for strain improvement and feed additive, food additive or

cosmetic manufacture

AUTHOR: SHIUAN D PATENT ASSIGNEE: SHIUAN D

PATENT INFO: US 2003104584 5 Jun 2003 APPLICATION INFO: US 2001-752957 2 Jan 2001

PRIORITY INFO: TW 2000-120972 7 Oct 2000; TW 2000-120972 7 Oct 2000

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: WPI: 2003-567956 [53]

ΤI

AB

=> s 14 and (biotin production)

0 L4 AND (BIOTIN PRODUCTION)

=> s 14 and (biotin)

8 L4 AND (BIOTIN)

=> d l6 ti abs ibib tot

ANSWER 1 OF 8 USPATFULL on STN L6

Whole cell engineering using real-time metabolic flux analysis The invention provides methods for whole cell engineering of new and modified phenotypes by using "on-line" or "real-time" metabolic flux analysis. The invention provides a method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis by making a modified cell by modifying the genetic composition of a cell and culturing the modified cell to generate a plurality of modified cells and measuring at least one metabolic parameter of the cell by monitoring the cell culture of in real time. The invention also provides articles comprising machine-readable medium including machine-executable instructions and systems, e.g., computer systems, to practice the

ACCESSION NUMBER: 2005:233489 USPATFULL

methods of the invention.

Whole cell engineering using real-time metabolic flux TITLE:

analysis

INVENTOR (S): Short, Jay M., Rancho Sante Fe, CA, UNITED STATES

Latterich, Martin, Montreal, CANADA

Levin, Michael, San Diego, CA, UNITED STATES Wei, Jing, San Diego, CA, UNITED STATES Fu, Pengcheng, Honolulu, HI, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2005202426	A1	20050915	
APPLICATION INFO.:	US 2003-491358	A1	20021001	(10)
	WO 2002-US31380		20021001	
			20050223	PCT 371 date

			NUMBER	DATE	
PRIORITY	INFORMATION:	US	2003-326653P	20011001	(60)
		US	2003-326654P	20011001	(60)
		US	2003-326655P	20011001	(60)
		US	2003-337526P	20011109	(60)

DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: DIVERSA C/O MOFO S.D., 3811 VALLEY CENTER DRIVE, SUITE

500, SAN DIEGO, CA, 92130, US

NUMBER OF CLAIMS: 80

EXEMPLARY CLAIM:

1

NUMBER OF DRAWINGS: 40 Drawing Page(s)

LINE COUNT: 4859

ANSWER 2 OF 8 USPATFULL on STN L6

TIScreening method for genes of brewing yeast

AB The present invention provides (A) a method for the selection of genes participating in the desired brewing character, which comprises preparing a database compiling the data of the whole genome sequence of industrial yeast, particularly a brewing yeast used for alcoholic beverages; selecting gene participating in a desired brewing character that the brewing yeast specifically possesses; and carrying out

functional analysis of the gene by disruption or overexpression; (B) a DNA array in which oligonucleotide(s) selected based on the data base compiling the data of the whole genome sequences of an industrial yeast, (C) a breeding method for constructing improved cultures achieving the desired brewing character, (D) a method for producing an alcohol or an alcoholic beverage in which productivity and quality are improved using the yeast, (E) a gene which is specific to the improved brewing yeast, and (F) a peptide encoded by the gene.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:334780 USPATFULL

TITLE:

Screening method for genes of brewing yeast

INVENTOR(S):

Nakao, Yoshihiro, Kyoto-shi, JAPAN Nakamura, Norihisa, Kyoto-shi, JAPAN

Kodama, Yukiko, Osaka, JAPAN Fujimura, Tomoko, Osaka, JAPAN Ashikari, Toshihiko, Osaka, JAPAN

PATENT ASSIGNEE(S):

SUNTORY LIMITED, OSAKA, JAPAN (non-U.S. corporation)

KIND DATE NUMBER -----

PATENT INFORMATION: US 2004265862 A1 20041230 APPLICATION INFO.: US 2004-791791 A1 20040304 (10)

NUMBER DATE JP 2003-57677 20030304

PRIORITY INFORMATION:

Utility

DOCUMENT TYPE:

FILE SEGMENT:

APPLICATION

LEGAL REPRESENTATIVE: BURNS DOANE SWECKER & MATHIS L L P, POST OFFICE BOX

1404, ALEXANDRIA, VA, 22313-1404 46

NUMBER OF CLAIMS:

1

EXEMPLARY CLAIM: NUMBER OF DRAWINGS:

12 Drawing Page(s)

LINE COUNT:

3038

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 3 OF 8 USPATFULL on STN

ΤI Whole cell engineering using real-time metabolic flux analysis AΒ

The invention provides methods for whole cell engineering of new and modified phenotypes by using "on-line" or "real-time" metabolic flux analysis. The invention provides a method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis by making a modified cell by modifying the genetic composition of a cell and culturing the modified cell to generate a plurality of modified cells and measuring at least one metabolic parameter of the cell by monitoring the cell culture of in real time. The invention also provides articles comprising machine-readable medium including machine-executable instructions and systems, e.g., computer systems, to practice the methods of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2004:44982 USPATFULL

TITLE:

Whole cell engineering using real-time metabolic flux

analysis

INVENTOR(S):

Fu, Pengcheng, Honolulu, HI, UNITED STATES

Latterich, Martin, San Diego, CA, UNITED STATES Levin, Michael, San Diego, CA, UNITED STATES

Wei, Jing, San Diego, CA, UNITED STATES

Short, Jay M., Rancho Santa Fe, CA, UNITED STATES Diversa Corporation, San Diego, CA (U.S. corporation)

PATENT ASSIGNEE(S):

NUMBER KIND DATE

\_\_\_\_\_\_\_\_ PATENT INFORMATION:

US 2004033975 A1 20040219 US 2002-264989 A1 20021001 (10) APPLICATION INFO.:

> DATE NUMBER

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PRIORITY INFORMATION:

US 2001-326655P 20011001 (60) US 2001-326654P 20011001 (60) US 2001-326653P 20011001 (60) US 2001-337526P 20011109 (60)

DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: GREGORY P. EINHORN, Fish & Richardson P.C., Suite 500,

4350 La Jolla Village Drive, San Diego, CA, 92122

NUMBER OF CLAIMS: EXEMPLARY CLAIM:

NUMBER OF DRAWINGS: 40 Drawing Page(s)

LINE COUNT: 5427

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 4 OF 8 USPATFULL on STN 1.6

тT Baker's yeast and a method producing it

A process is disclosed for the production of baker's yeast which AB comprises the fermentation of a baker's yeast strain using a non-molasses carbon source until a fermentation broth having at least 10%, preferably at least 13%, more preferably at least 16% of dry solids

content is formed, which can be used directly as a cream yeast without concentration.

ACCESSION NUMBER:

1999:72304 USPATFULL

TITLE:

Baker's yeast and a method producing it

INVENTOR(S): PATENT ASSIGNEE(S):

Plomp, Pieter Jan Arnoldus Maria, Ex Delft, Netherlands Gist-brocades, B.V., Netherlands (non-U.S. corporation)

NUMBER KIND DATE -----US 5916609 19990629

PATENT INFORMATION: APPLICATION INFO.:

19970728 (8) US 1997-901312

NUMBER DATE -----

PRIORITY INFORMATION: DOCUMENT TYPE:

EP 1996-202119 19960727 Utility

FILE SEGMENT: Granted

FILE SEGMENT: Granted
PRIMARY EXAMINER: Sayala, Chhaya D.

LEGAL REPRESENTATIVE: Morrison & Foerster, LLP

NUMBER OF CLAIMS: 21 EXEMPLARY CLAIM: 1 LINE COUNT: 537

1.6 ANSWER 5 OF 8 USPATFULL on STN

ТT Production of distillers yeast

AB Distillers yeast is produced by a process which results in more rapid yeast growth, higher cell concentrations and greatly extended yeast viability. The process involves propagating yeast on a culture medium of cooked cereal grain mash which has been subjected to enzymatic action of glucamylase obtained from fungi of the genus Aspergillus. After propagation, as a result of substantially longer viability, the yeast can be stored in the culture medium for up to 3 days or longer with portions being withdrawn from time to time for inoculating distillery grain mashes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

75:10033 USPATFULL

TITLE:

Production of distillers yeast

INVENTOR (S):

Van Lanen, deceased, James M., late of Peoria, IL,

United States

Smith, Merritt B., Peoria, IL, United States Maisch, Weldon F., Peoria, IL, United States

PATENT ASSIGNEE(S):

Hiram Walker & Sons, Inc., Peoria, IL, United States

(U.S. corporation)

NUMBER KIND DATE

PATENT INFORMATION:

APPLICATION INFO.:

RELATED APPLN. INFO.:

US 3868307 19750225 US 1973-388359 19730815 Continuation-in-part of Ser. No. US 1971-189678, filed

on 15 Oct 1971, now abandoned

DOCUMENT TYPE:

FILE SEGMENT:

Granted Naff, David M.

PRIMARY EXAMINER: LEGAL REPRESENTATIVE:

Kirkland and Ellis

NUMBER OF CLAIMS:

EXEMPLARY CLAIM:

1

NUMBER OF DRAWINGS:

2 Drawing Figure(s); 2 Drawing Page(s)

LINE COUNT:

633

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 6 OF 8 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

Bread-baking yeast preparation - involves adding aryl-thioacetic acid derivs. TIto des thio-biotin used in molasses-based nutrient medium for yeast cultivation.

1988-159690 [23] WPIDS AN

1350172 A UPAB: 19930923 AB

The bread-baking yeasts are obtd. by multistage cultivation under aeration conditions on a nutrient medium containing molasses, mineral salts and desthiobiotin. During the stages of production of yeast inoculant and commercial yeasts, derivs. of arylthio (sulphonyl) acetic acid are added in amount (1-10000)x10 power minus 10% jointly with desthiobiotin.

The specified derivs. are 2-hydroxyalkyl-ammonium salts of formula (I), where (a) R=H, R2=4CH3, n=2 and X=N+H3CH(CH2OH)CH(OH)C6H4NO2-4; (b) R1=H, R2=4Cl, n=O and X=N+H(CH3)2CH2CH2OH; or (c) R1=H, R2=4Cl, n=2, and X=N+H (CH2CH2OH) 3.

(I) contain metabolically active sulphur which can be incorporated into desthiobiotin and form biotin. (I) also act as antioxidants by lowering the intensity of peroxide oxidation of lipids of biological membranes.

USE/ADVANTAGE - In the microbiological industry. Increased biomass yield is obtd. Bul.41/7.11.87

0/0

ACCESSION NUMBER:

1988-159690 [23] WPIDS

DOC. NO. CPI:

C1988-071563

TITLE:

Bread-baking yeast preparation - involves adding aryl-thioacetic acid derivs. to des thio-biotin used in molasses-based nutrient medium for yeast

cultivation.

DERWENT CLASS:

D11 D16 E19

INVENTOR(S): PATENT ASSIGNEE(S): GUSEVA, S A; LEVKOVSKAY, G G; MIRSKOVA, A N (ASII) AS SIBE IRKUT ORG CHEM; (BREA) LENGD BREAD BAKING

COUNTRY COUNT:

1

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG \_\_\_\_\_\_ SU 1350172 A 19871107 (198823)\* 3

#### APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
	- <b></b>		
SU 1350172	A	SU 1985-3960649	19851005

PRIORITY APPLN. INFO: SU 1985-3960649 19851005

L6 ANSWER 7 OF 8 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

TI Yeast prepared by culturing Hansenula ofunaensis - in medium containing methanol, ethanol and/or glucose as carbon source.

AN 1978-02953A [02] WPIDS

AB JP 52139773 A UPAB: 19930901

The method is characterised by culturing a novel yeast stock Hansenula of unaensis (FERM-P 3494). The yeast stock Hansenula of unaensis can utilise methanol, ethanol and glucose, which are favourable as the starting material for preparing yeast for food use.

The culture is practiced aerobically at 10-41 pref. 30-39 degrees C in the medium containing methanol, ethanol and/or glucose as carbon source at pH 2-9 pref. 3-7 for up to 6 days. As the growth promoter vitamins such as thiamine, biotin, etc. and amino acid such as methionine, cysteine, etc. can be applied. After the culture yeast body is separated washed and dried.

ACCESSION NUMBER:

1978-02953A [02] WPIDS

TITLE:

Yeast prepared by culturing Hansenula ofunaensis - in

medium containing methanol, ethanol and/or glucose as carbon

source.

DERWENT CLASS:

C03 D13 D16

PATENT ASSIGNEE(S):

(MITK) MITSUI TOATSU CHEM INC

COUNTRY COUNT:

PATENT INFORMATION:

PA	TENT NO	KII	ND DATE	WEEK	LA	PG
JP	52139773	A	19771121	(197802)*		
JΡ	56012109	В	19810318	(198115)		

PRIORITY APPLN. INFO: JP 1976-44940 19760422

- L6 ANSWER 8 OF 8 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
- TI Yeast preparation using Torulopsis methanothermophilus in culture medium containing methanol as carbon source and **biotin**.
- AN 1977-19283Y [11] WPIDS
- AB JP 52015882 A UPAB: 19930901

Method is effected by inoculating a stock belonging to Torulopsis methanothermophilus which can utilize methanol, into a culture medium containing methanol as carbon source and **biotin**, culturing it for multiplication and separating the yeast body.

The stock can multiply at high temperature and low pH and is considered a novel stock. The stock is trusted to Institute of Microbial Industry with the Trust Number 3158. As teh carbon source crude methanol which contains small amount of lower aldehydes, lower alcohols, etc. can be used. With methanol concentrate >4% the growth of the yest is inhibited, so methanol is added to the culture medium little by little.

ACCESSION NUMBER:

1977-19283Y [11] WPIDS

TITLE:

Yeast preparation using Torulopsis methanothermophilus - in

culture medium containing methanol as carbon source and

biotin.

DERWENT CLASS:

D16

PATENT ASSIGNEE(S): (MITP) MITSUBISHI PETROCHEMICAL CO LTD

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG -----

JP 52015882 A 19770205 (197711)\*

PRIORITY APPLN. INFO: JP 1975-91807 19750728

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(FILE 'HOME' ENTERED AT 13:07:27 ON 20 SEP 2005)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, BIOSIS, BIOTECHDS'

ENTERED AT 13:08:15 ON 20 SEP 2005

272 S (INTEGRATING PLASMID) L1

5634 S CANDIDA UTILIS L2

L311 S L2 AND (BIOTIN SYNTHASE)

310 S YEAST PREPARATION L4

0 S L4 AND (BIOTIN PRODUCTION) L5

8 S L4 AND (BIOTIN) L6

=> s 11 and 13

0 L1 AND L3 L7

=> s 12 and 11

L8 2 L2 AND L1

=> d 18 ti abs ibib tot

ANSWER 1 OF 2 USPATFULL on STN 1.8

TI Production of farnesol and geranylgeraniol

AB The invention provides a biological method of producing farnesol or geranylgeraniol.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:144592 USPATFULL

TITLE: INVENTOR(S):

Production of farnesol and geranylgeraniol Millis, James R., Kohler, WI, UNITED STATES

Maurina-Brunker, Julie, Appleton, WI, UNITED STATES McMullin, Thomas W., Manitowoc, WI, UNITED STATES

PATENT ASSIGNEE(S):

Arkion Life Sciences LLC. (U.S. corporation)

NUMBER KIND DATE -----PATENT INFORMATION: US 2004110257 A1 20040610 US 2003-719196 A1 20031120 (10) APPLICATION INFO.:

RELATED APPLN. INFO.:

Continuation of Ser. No. US 2001-909558, filed on 20 Jul 2001, GRANTED, Pat. No. US 6689593 Continuation of Ser. No. US 1999-350275, filed on 6 Jul 1999, GRANTED,

Pat. No. US 6531303

DATE NUMBER -----PRIORITY INFORMATION: US 1998-91964P 19980706 (60)

DOCUMENT TYPE:

Utility

FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: SHERIDAN ROSS PC, 1560 BROADWAY, SUITE 1200, DENVER,

CO, 80202

NUMBER OF CLAIMS: 17 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 11 Drawing Page(s)

LINE COUNT: 3450

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L8 ANSWER 2 OF 2 USPATFULL on STN

TI Manufacture of five-carbon sugars and sugar alcohols

AB The invention relates to the methods of manufacturing five-carbon sugars

and sugar alcohols as well as other compounds derived from

pentose-phosphate pathway from readily available substrates such a

hexoses using metabolically engineered microbial hosts.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2003:99684 USPATFULL

TITLE:

Manufacture of five-carbon sugars and sugar alcohols

INVENTOR(S):

Miasnikov, Andrei, Kantvik, FINLAND Ojamo, Heikki, Kirkkonummi, FINLAND Povelainen, Mira, Espoo, FINLAND Gros, Hakan, Kantvik, FINLAND Toivari, Mervi, Espoo, FINLAND Richard, Peter, Helsinki, FINLAND

Richard, Peter, Helsinki, FINLAND Ruchonen, Laura, Helsinki, FINLAND Koivuranta, Kari, Helsinki, FINLAND Londesborough, John, Helsinki, FINLAND Aristidou, Aristos, Espoo, FINLAND Penttila, Merja, Helsinki, FINLAND Plazanet-Menut, Claire, Paris, FRANCE

Deutscher, Josef, Fontenay Le Fleury, FRANCE

PATENT ASSIGNEE(S):

Xyrofin Oy (non-U.S. corporation)

APPLICATION INFO.: RELATED APPLN. INFO.:

PATENT INFORMATION:

Continuation-in-part of Ser. No. US 2000-488581, filed on 21 Jan 2000, ABANDONED Continuation-in-part of Ser. No. US 1997-790585, filed on 29 Jan 1997, PENDING Continuation of Ser. No. US 1995-368395, filed on 3 Jan

Continuation of Ser. No. US 1995-368395, filed on 3 Jan 1995, GRANTED, Pat. No. US 5631150 Continuation of Ser. No. US 1993-110672, filed on 24 Aug 1993, ABANDONED Continuation-in-part of Ser. No. US 1992-973325, filed on 5 Nov 1992, ABANDONED Continuation-in-part of Ser.

No. WO 2001-FI51, filed on 22 Jan 2001, UNKNOWN

DOCUMENT TYPE: Utility

FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC, 1100 NEW YORK

AVENUE, N.W., SUITE 600, WASHINGTON, DC, 20005-3934

NUMBER OF CLAIMS: 166

EXEMPLARY CLAIM: 1

25 Drawing Page(s)

LINE COUNT: 5422

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> file scisearch, biosis, medline, uspatful, wpids, biotechds, embase, dgene

COST IN U.S. DOLLARS

NUMBER OF DRAWINGS:

SINCE FILE

ENTRY SESSION

FULL ESTIMATED COST

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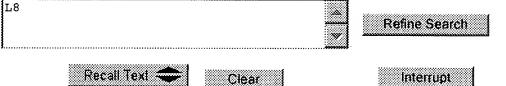
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Terms	Documents
L7 and L1	1

US Pre-Grant Publication Full-Text Database US Patents Full-Text Database US OCR Full-Text Database Database: EPO Abstracts Database JPO Abstracts Database **Derwent World Patents Index** 

IBM Technical Disclosure Bulletins

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### Search History

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<u>L7</u>	L6 and (saccharomyces cerevisae)	23150	<u>L7</u>
<u>L6</u>	L5 and (cycloheximide-resistance gene)	73128	<u>L6</u>
<u>L5</u>	L4 and (yeast preparation)	76057	<u>L5</u>
<u>L4</u>	L2 and integrating plasmid	82646	<u>L4</u>
<u>L3</u>	L2 and l1	3	<u>L3</u>
<u>L2</u>	candida utilis biotin synthase	79111	<u>L2</u>
<u>L1</u>	shiuan.in.	76	<u>L1</u>

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sing default format became				
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GPUB-DOCUMENT-NUMBER: GPUB-FILING-TYPE: new DCUMENT-IDENTIFIER: U	N .			•
TLE: Yeast with high	n biotin-productivi	ty and the <u>pr</u>	eparation metho	od thereof
BLICATION-DATE: June	e 5, 2003			
VENTOR-INFORMATION:				•
AME	CITY	STATE	COUNTRY	RULE-47
niuan, David	Kaohsiung		TW	
-CL-CURRENT: <u>435/119</u>	9; <u>435/254.2</u> , <u>435/3</u>	<u>20.1, 435/483</u>		
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L7 and L1				1

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1. Document ID: US 20030104584 A1

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L3: Entry 1 of 3

File: PGPB

Jun 5, 2003

PGPUB-DOCUMENT-NUMBER: 20030104584

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030104584 A1

TITLE: Yeast with high biotin-productivity and the preparation method thereof

PUBLICATION-DATE: June 5, 2003

INVENTOR-INFORMATION:

NAME CITY

Ϋ́

STATE COUNTRY

RULE-47

Shiuan, David

Kaohsiung

TW

US-CL-CURRENT: 435/119; 435/254.2, 435/320.1, 435/483

Full Title Citation	n Front Revis	oo Classification	Date	Reference	Sequences	Attachments	Claims	KANC	Draw Desc	ima
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2. Document ID: US 20030003549 A1

L3: Entry 2 of 3

File: PGPB

Jan 2, 2003

PGPUB-DOCUMENT-NUMBER: 20030003549

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030003549 A1

TITLE: DETECTION OF HUMAN HEPATITIS B VIRUS SURFACE ANTIGEN MUTANTS BY SPECIFIC

AMPLIFICATION AND ITS APPLICATION ON GENE CHIP

PUBLICATION-DATE: January 2, 2003

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47 OON, CHONG-JIN SINGAPORE SG CHEN, WEI-NING SINGAPORE SG LEONG, AI-LIN SINGAPORE SG KOH, SHIUAN SINGAPORE SG

US-CL-CURRENT: <u>435/110</u>

Full Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc
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3. Document ID: US 6759193 B2

L3: Entry 3 of 3 File: USPT Jul 6, 2004

US-PAT-NO: 6759193

DOCUMENT-IDENTIFIER: US 6759193 B2

TITLE: Detection of human hepatitis B virus surface antigen mutants by specific

amplification and its application on gene chip

DATE-ISSUED: July 6, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Oon; Chong-Jin	Singapore			SG
Chen; Wei-Ning	Singapore			SG
Leong; Ai-Lin	Singapore			SG
Koh; <u>Shiuan</u>	Singapore			SG

US-CL-CURRENT: 435/6; 435/5, 435/91.2, 536/23.72, 536/24.3, 536/24.33

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                                                                                                                                E.coli Bio
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Direct Submission
Submitted (05-DEC-1999) Graduate Institute of Biochemistry,
100, Shih-Chuan 1st Road, Kaohsiung, Taiwan
Location/Qualifiers
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2 (bases 1 to 5278)
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gtpmaebladpkskklofdbellrtiataarivmpkaiirlaagrytmketbgpevcfmag
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Submitted (14-MAX-1996) Data collected by MIPS on behalf of the Submitted (14-MAX-1996) Data collected by MIPS at the European yeast chromosome VII sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Maxtinsried, FRG; E-mail: Mewes@mips.embnet.org
Location/Qualifiers
1. 4068
                                                                                               GTTAAGAACAAGCAAGTTGAAGTTGATGATGACTGTCAGAACCATTGCTACTGCAAGATTG
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GGTGAGACCCAAGAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCAT
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Voet, M. and Volckaert, G.
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     IMKEAEQVMCFMAGCNAIFTGKKMLTTMCNGWDEDKAMLAKWGLKPMESFKYKPREVA
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                                                                                                                                                                                                                                                                                                                        Length 5278;
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 1188; DB 8;
.larity 100.0%; Pred. No. 1.5e-308;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                   LKPMESFKYKPREVAFGA
                                            1044. .5102
'gene="Bio2"
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 1188; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAGGAAATGGTGACCAAAGTGAATGATATGGGGCTAGAAACGTGTGTTACTTTAGGTA 16182
                                                                                                  PLN 14-APR-1997
                                                                                                                                                                                                                                                                                             Volckaert,G., Voet,M. and Robben,J.
Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the Sequence analysis of a near-subtelomeric 35.4 kb DNA segment or the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MALI locus reveals IS complete open reading frames, including ZUOI, BGL2 and BIO2 genes and an ABC transporter gene 774sest 13 (3), 251-259 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted (14-DEC-1995) G. Volckaert, Laboratory of Gene
Technology, Catholic University of Leuven, Willem de Croylaan 42,
B-3001 Leuven, BELGIUM
Location/Qualifiere
                                                                                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTATCATACCCCACTGCTCGAACTTACTCATGCAGCACAATTGCAGCACAGAAAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15943 AGGACTGTAAGTATTGTGCGCAGTCTTCGAGAAACGATACCGGTCTAAAGGCTGAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTCTGCCTAGGTGCTGCATGGAGAGACATGAAAGGTCGTAAATCAGCCATGAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATATGCATTGTCAGTGAAGACACCAGTCAACACCTGGACCAAAGAAGAAATTAAAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 TATATGACACACCACCACTCATGGACTTGATGCACTCAGGTGCAACACACAGGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAACCTTCAGAGGTTCAATTGTGCACTCTTATGAATATCAAAACTGGTGGTTGTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AGGACTGTAAGTACTGTGCCCAATCACAGCGTTACAACACTGGTGTCAAGGCTGAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATCCAAGTTGATGAGGTGATTGAAGCTGCAAAGGAGGCAAAGGCCCAATGGATCTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="right arm"
/clone="cosmid pEGH452"
/clone_lib="H.Tettelin (Louvain-la-Neuve, Belgium)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                DNA linear
chromosome VII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae"
  AATGGGGATTGCAACCTATGGAGGCATTTAAGTACGA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 519.4; DB 8;
Pred. No. 1.4e-128;
0; Mismatches 281;
                                                                                                                                                                                                   cerevisiae (baker's yeast)
                                                                                                S5400 bp cerevisiae DNA for fragment from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Saccharomyces
/mol_type="genomic_DNA"
/strain="FY1679"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4932"
/chromosome="VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 35400)
Volckaert, G.
Direct Submission
Submitted (14-DEC-1995) G.
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Matches 707;
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SOURCE
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                                                                                                                                                                                                                                                        TTTATCATACCCCACTGCTCGAACTTACTCATGCAGCACAATTGCAGCACAGAAGTGGC 1547
                                                                                                                                                                                                                                                                                                                                      ACGATCCAACCAAAGTGCAATTGTGCACATTGATGAACATCAAATCTGGTGGTTGTTCTG 1487
                                                                                                                                                                                                                                                                                                                                                                                                          AGGACTGTAAGTATTGTGCGCAGTCTTCGAAACGATACCGGTCTAAAGGCTGAGAAAA 1427
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                                                                                                                                       AATATGCATTGTCAGTGAAGACACCAGTCAACACCTGGACCAAAGAAGAAATTAAAGCTA 232
                                                                                                                                                                                                                     292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATGAAAGAGCAGAACAGGTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAG 1063
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                                                       Score 519.4; DB 8;
Pred. No. 1.5e-128;
0; Mismatches 281;
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Best Local Similarity 70.9%;
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I (bases I to 1847)
Zhang, S., Sanyal, I., Bulboaca; G.H., Rich, A. and Flint, D.H.
The gene for biotin synthase from Saccharomyces cerevisiae:
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                           GACTGTAAGTACTGTGCCCAATCACAGCGTTACAACACTGGTGTCAAGGCTGAAAGAATC
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Saccharomyces cerevisiae
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    TGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACATA
                                                         ACATTGATACTTACAAGGAACACTATCCAAAGGTGATCTCCCACAAGAAGCTTTGATGATA
                                                                                                            GATTGAAAACATTCAAAAACGTTCAAGGATCTGGATTAAAGGCATGCACAGGTGGTATTC
                                                                                                                                                                 TTGGTCTTGGTGAGACCCAAGAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGG
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Pred. No. 7.4e-117;
0; Mismatches 317; Indels
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                                                                                                                                                          Biology,
MA -2139, USA
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  complementation of Escherichia coli
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Zheng, 16-739 Dept. of
Massachusetts Institute of Technology, Cambridge,
Location/Qualifiers
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Pred. No. 3.2e-116;
0; Mismatches 294; Indels
  cloning, sequencing, and complementation of E
strains lacking biotin synthase
Arch. Biochem. Biophys. 309 (1), 29-35 (1994)
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/organism="Saccharomyces
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/strain="20B-12"
/db_xref="taxon:4932"
/chromosome="VII"
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/gene="BIO2"
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/gene="BIO2"
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85099 TGGGACGAGGATAAGGCCATGCTGGAGAAGTGGGGACTGAAGCCCATGAAGAGCTT 85154
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Pred. No. 2.4e-110;
0; Mismatches 339;
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WPCOMMENT
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                                                                                                                                                                                                Indels
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Pred. No. 2.8e-112;
0; Mismatches 297;
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Wood, V., Gwilliam, R., Rajandream, M.A., Lyme, M., Lyne, R.,
Stewart, A., Sgouros, J., Peat, N., Hayles, J., Baker, S., Basham, D.,
Buwman, S., Brooks, K., Brown, D., Brown, S., Chillingworth, T.,
Churcher, C., Collins, M., Connor, R., Cronin, A., Hawilh, T.,
Falstwell, T., Fraser, A., Gentles, S., Gobbe, A., Hawlin, N., Harris, D.,
Hudalo, J., Hodgson, G., Jagels, K., James, K., Jones, L., Jones, M.,
Leather, S., McDonald, S., McLean, J., Mooney, P., Moule, S.,
Mungall, K., Murphy, L., Niblett, D., Odell, C., Oliver, K., O'Neil, S.,
Bearson, D., Quall, M.A., Rabbinowitech, E., Rutherford, K., Rutter, S.,
Saunders, D., Seeger, K., Sharp, S., Skelton, J., Simmonds, M.,
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   AGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGCCATGAC---CT
                            AGGAAGAAAGTCTGCCTTAGACAAAATCAGTAAAGTTGTTAAACAAATCAACGAGGTT
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                                                                    564 TGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAA
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                                                                                                                                     AAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAA
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Schizosaccharomyces pombe
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30334
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                                                                                                                                                                                     ATTGGTCATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGC 1016
                                                                                                                                                                                                                                                                                                                             1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1263)
Weinstock,K.G. and Bush,D.
Nucleic acid sequences relating to Candida albicans for diagnostics
and therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAA 446
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                                                                                                                                         AATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGTTAAGA-----
                                                                                                                  ------ACAAGCAAGTTGAAGTTGAGATTGTCAGAACCATTGCTACAAG
                                                                                                                                                                                                                                                          AGAACAGGTGATGTCCTTCATGCCTGGTTGTAATGCCATCTTCACAGGTAAGAAATGCT
                                                                                                                                                                                                                                                                                         30273 TGAGCAATTCTTATGTTTCATGAGTGGTTGTAACGCTATCTTCACGGTGAAAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                            ACCAATGGAGAGTTTCAAATACAAACCAAGGGAGGT 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.9%; Score 414.4; DB 6; 66.8%; Pred. No. 2.8e-100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp DNA
6747137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: US 6747137-A 4445 08-JUN-2004;
Location/Qualifiers
1. 1263
/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'mol_type="genomic DNA"
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4445 from patent US
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AR549314
AR549314.1 GI:53942489
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Best Local S
Matches 643
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SOURCE
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TITLE

COMMENT

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with=SPTR:; date=20030609
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3770. .380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,
Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,
Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Waltjens,I.,
Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,
Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,
Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,
Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,
Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,
Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,
Ussery,D., Barrell,B.G. and Nurse,P.
The genome sequence of Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and AGOWA GmbH, Glienicker Weg 185, D-12489 Berlin, Germany On Apr 14, 1999 this sequence version replaced gi:2995362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(URL, http://www.ganedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S.pombe/)

CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (circomosome 1), c5H10 (coemid name), .01 (first CDS), c pombe), A (circomosome 1), c5H10 (coemid name), .01 (first CDS), c lcomplementary strand) However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference. IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once location.

    .7687
/note="nominal overlap with cosmid SPCC330, EM:AL031603 S.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood, V., Rajandream, M.A., Barrell, B.G., Wedler, H., Wambutt, R. and Wedler, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aspect=P; term=threonine catabolism; GOid=GO:0006567;
evidence=ISS; db_xref=GOC:unpublished; with=SPTR:P05792;
date=20030609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aspecter; term=branched chain family amino acid
biosynthesis; GOid=GO:0009082; evidence=ISS;
db_xref=GOC:unpublished, with=SPTR:; date=20030609
aspect=F; term=threonine dehydratase activity;
GOid=GO:0004794; evidence=ISS; db_xref=GOC:unpublished;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   threonine catabolism, involved in branched chain amino acid biosynthesis, threonine dehydratase activity;
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Complement (709. .1680)
/gene="sPCC30.14"
/Ec number="4.3.1.19"
/note="threonine_dehydratage_(predicted); involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    localization unknown; similar to S. cerevisiae YKL218C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-MAR-1998) Buropean Schizosaccharomyces genome
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/note="rpl242 see c330 for full length CDS"
coche="rpl242 see c330 for full length CDS"
/gene="spcc320.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .40005
/organism="Schizosaccharomyces pombe"
/mol_type="genomic DNA"
/strain="972h-"
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/chromosome="III"
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MEDLINE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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FEATURES

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/note="serine/threonine protein kinase; aurora homolog; involved in spindle checkpoint; involved in spindle formation (required) (PMID 1192803); involved in sister chromatid separation (required) (PMID 11950927); involved in the microtubule attachment response (required) (PMID 12676091); interacts physically and/or genetically with the inner centromere protein Picip (PMID 11950927); interacts physically and/or genetically with the inner centromere protein Picip (PMID 11950927); interacts physically and/or genetically with survivin (PMID 11950927); involved in protein amino acid phosphorylation (SERIO Of Hht3p) (PMID 11792803); similar to S. cerevisiae
                                                                                                                                                                                                                     / LTATA 14 L. 10n= "MSDNLVLPTYDDVASASER!KKPANKTPVLTSSTVNKEFVABVF
PKCENFQKMGAFKFRGALNALSQLNBAQRKAGVLTFSSGNIAQAIALSAKILGIPAKI
IMPLDAPEAKNAATKGYGGYIMYDRYKKYBORREMAKEISERECLIIIPPYDHPHVLAG
QGTAAKELFEEVGPLDALFYCLGGGGLLSGSALAAHFAPNCEVYGVBPEANBGQS
FRKGSIVHIDTPKTITADGAQYQHIGNYTFS!IKEKVDDILIYSDEBLIDCLKFYAARN
KIVVEPTGCLSFAAARAMKEKLKNKRIGIIISGGNVDIERYAHFLSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSDSKLADSLNCLSVSTPSTTANPGRQQLLRLAVSNQRQVNNVS
LANGKENKRTSNSKFNSSLRKIEEPIAGVPSSAGPQWREFHIGMFEIGKPLGKGKFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYLAKEKKTGFIVALKTLHKSELVQSKIEKQVRREIEIQSNLRHKNILRLYGHFHDEK
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LAGIGGEIKASDFKGWSVHABSORRTTLCGTLDYLPPEMVEGKEHTEKVDLWSLGVLIY
EFIVGAPPFEDMSGATYKRIAKVDLKIPSFVPPDARDLISRLLQHNFEKRMSLEGV
MRHPWIVKYKDSWTRKSSESS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="synonyms: sex1, SPCC320.13c, SPCC330.16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Pfam match to entry S_T_dehydratage ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08.01.3003 trimmed to 2nd met PMID 12676091"
component unknown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes"tRNA Glutamic acid
tRNA Glu anticodon CTC, Cove score 74.15"
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complement (join (4707. .4714,4781. .5330))
/gene="SPCC320.12"
/note="SPCC340.17"
complement (join (4707. .4714,4781. .5330))
                                                                                         /protein_id="CAA18316.1"
| db_xref="G12995376"
| db_xref="G0A:059791"
| db_xref="UniProt/Swiss-Prot:059791"
aspect=C; term=cellular compone
GOid=GO:0008372; date=20030609"
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/protein_id="CAD88264.1"
/db_xref="GI:29786364"
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prot ein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1123. .1518)
/gene="SPCC320.14"
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/gene="SPCTRNAGLU.09"
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/gene="SPCTRNAGLU.09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="tRNA-Glu"
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                                                                    codon start=1
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/gene="ark1"
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/gene="ark1"
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/gene="ark1"
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/gene="ark1"
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742 TCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGT
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Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38684 CGCTACAATACCGGTGTCAAGGCCACTAAGCTCATGAAATTGACAAGTTTTGGAAAAG 38743
                                                                                                                        /protein id="CAA18314.1"
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/tb_xref="UniProt/Therbi.059789"
/tb_xref="UniProt/Therbi.059789"
/tb_xref="UniProtVirgal"
/tb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38744 GCTAAAATTGCAAAGGCTAAAGGAAGCACTAGATTTTGTATGGGAAGTGCCTGGCGTGAT 38803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38924 AAGGATGCAGGCTTGACGGCATACAATCATAATCTTGATACCTCTCGCGAATATTACTCA 38983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38984 AAGATTATCAGCACTAAGGACATATGATGAACGGTTAAATACTATTGACAATCTTCGGAAA 39043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38864 ATGGATATGGAAGTTTGCGTAACCCTTGGTATGTAAATGAACAGCAAGCCAAGGAACTA 38923
                              metallopeptidase (predicted); similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AACACCTGGACCAAAGAAGAAATTAAAGCTATATATGACACCCCACCATGGACTTGATG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAG 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4775. .4780)

/gene="SPCG320.12"
/note="gtacgt, splice donor sequence"
complement (5055. .5084)
/gene="SPCG320.12"
/note="SPCG320.12"
/note="PS00142 Neutral zinc metallopeptidages, zinc binding region signature"
join(5867. .5922,6076. .6162,6325. .6724)
/gene="SPCG320.11c"
/note="SPCG320.11c"
/oodon_start=1
/codon_start=1
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/db_xref="UniProt/TrEMBL:059788"
                                  note="neutral zinc metal
o S. cerevisiae YNR020C"
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/db_xref="GI:2995373"
                                                                                                                                                                                                                                                                                                                                                          complement (4715. .4738)
/gene="SPCC320.12"
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Stewart, A., Squoros, J., Peat, N., Hayles, J., Baker, S., Basham, D., Bewartha. Squoros, J., Peat, N., Hayles, J., Baker, S., Basham, D., Bowman, S., Brooks, K., Brown, D., Brown, S., Chillingworth, T., Churcher, C., Collins, M., Connor, R., Cronin, A., Davis, P., Churcher, C., Collins, M., Connor, R., Goble, A., Hamlin, N., Harris, D., Hidalgo, J., Hant, S., Jagels, K., Jagels, K., Janes, M., Howarth, S., Huckle, E.J., Hunt, S., Jagels, K., Jagels, K., Jones, L., Jones, M., Leather, S., McDonald, S., McLean, J., Mooney, P., Moule, S., McDonald, S., McDent, D., Odell, C., Ollver, K., O'Neil, S., Squares, S., Stevens, K., Taylor, K., Taylor, R., Taylor, R., Squares, D., Seeger, K., Starop, S., Skelton, J., Simmonds, M., Squares, S., Stevens, K., Taylor, R., Taylor, R., Taylor, R., Taylor, R., Taylor, R., Taylor, R., Gabel, C., Volckaert, G., Aert, R., Robben, J., Grymonprez, B., Weltfens, J., Walsh, S., Warren, T., Whitehead, S., Woodward, J., Volckaert, G., Aert, R., Robben, J., Grymonprez, B., Weltfens, T., Hilbert, H., Borzym, K., Langer, M., Schafeer, M., Wuller-Auer, S., Gabel, C., Holzer, B., Mostel, D., Hilbert, H., Borzym, K., Langer, H., Schafeer, M., Weller, H., Borzym, K., Langer, J., Lehrach, H., Waller, R., Pohl, T. M., Eder, P., Zimmermann, W., Wedler, H., Hut, C., Moore, K., Hurst, S.M., Lucas, M., Rochet, M., Gallbart, F., Denander, S., Lelaure, V., Mottlets, S., Mallbert, P., Potrashkin, J., Shpakovski, G.V., Ussery, D., Barrell, B.G. and Nurse, P., Lowe, T., McComble, W.R., Paulsen, I., Potrashkin, J., Shpakovski, G.V., Lowe, T., McComble, W.R., Paulsen, I., Potrashkin, J., Shpakovski, G.V., Ussery, D., Barrell, B.G. and Nurse, P.
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                                                                                                                                                                                                                  39104 GTAGGATTGATTCACTCGTTAGCAACTATGCCAACACCATCCTGAATCTGTACCCTTTAAT 39163
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39044 GCTGGGTTGAAGGTTTGTAGCGGTGGTATTTTGGGTCTAGGGGAGAAAAGCATGATCGT
                                                                                                               802 GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAAC
                                                                                                                                                                                                                                                                                                                            GITGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMGSSSNNSNSSNNNSNTSNNNSNTSNNESMYSKLSSLSGMASSFLGSSGNNNNNNNS
NSGNYNNNNSGNNNQOHQQSSSSLQCLASSFLNSSSGNSNKQNYNNNNNQNYGNNNNQ
NYNNNNNSSQGGNSQGGSGLLGQAVNMFLKS"
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SIHRKFHDPKKVQQCTLLSIKTGGCTEDCKYCAQSSRYNTGVKATKLMKIDBVLEKAK
AKAKGSTRFCMGSAWRDLNGRNRTPKNILBIIKEVRSMDMBVCVTLGMLNBQQAKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDAGLTAYNHNLDTSREYYSKIISTRTYDERLNTIDNLRKAGLKVCSGGILGLGEKKH
DRVGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKERLPIHPFLRSIATARICMPK
TIIRPAAGRNTCSESEQALAFMAGANAVFTGEKMLTTPAVSWDSDSQLFYNWGLEGMQ
                                                                                                                                              Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL,

ttp://www.sanger.ac.uk/Projects/S_pombe/)

CDS are numbered using the following system eg SPACSH10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), ol (first CDS), c

[complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference. IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once. Location/Qualifiers

    .2935
'note="nominal overlap with cosmid SPCC320, EM:AL022245 S.

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                         Direct Submission
Submitted (28-SEP-1998) European Schizosaccharomyces genome
sequencing project, Sanger Institute, The Wellcome Trust Genome
Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk
Rajandream, M.A., Barrell, B.G., Murphy, L. and Harris, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="sylonyms: SPCC1235.02, SPCC320.01c"
1374. .2465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |db_xref="GOA:O59778"
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chromosome="III"
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/gene="SPCC1235.03"
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gene="SPCC1235.03"
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/gene="bio2"
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  AUTHORS
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AKDTGLSLKICTDVLICSNDYKNALWILCLIKETOHNEMGNIKLSSOTAKSNSSTQTK
TCTNODOSKLVUDDDFALSABDCNRLAESYLELNMOYSNSAKTSRRSKSNHLFGGSAM
YHAOLGERYHEKALKYSLLAMRSLAHSGTSHSLDLHGATVREAKTIVREKVAMWAKE
ADTSPNSIRPVIVTGRGNHSIGLEARLLPAIVRLLOODHWRFDAEHGQLITVYGINRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /procein id="CAA21108.1"
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INNNFGYSYUGQSSQPVPSYNPLPSYNTASLPNAGIPAAMPGMPSGYFGTVPIPQGGY
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TQRSRSSSANPVTTPPVNNTLLTPPAPPVELPPVTTTSPNAIIRSVQMIRSFVPQAPI
HQVINTLAQTKWDETAALSIISQKYLSCDLGIPIQEHKRFKQSPVASNMPTYGSSNRT
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RDTSALERTVLNFINSTAKELSDTASCPLSHSKLLLEHRPFQTLAEACIIKHPDDVP
SKPGRRGRRFEKNPMGQXIVNACMETWBGYYAIDNLIAKCEFLGNRISKGMASWGIKL
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RVEPYYGSQQERANIREAIEENEIKYDILVTTYQLATNNKEDRSFLKHQNFDVCVYDB
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LFRKFYDDEKLKOMAKDIMOEBOYKNANBOYIYEDMEVMSDFELHRLCRSFPTLOSYT
LKDDPMMDSGKIRVLKELLPKMKEBGSRILLFSQFTOMLDILEQVLDTLKISYVRLDG
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/gene="SPCC1235.04c"
/note="ctaacgtttattacaag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPCC1235.03"
/note="mRNA from SPD171"
complement(join(5485. .5736,5785. .6193,6247. .6383))
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/note="DEAD/DEAH box helicase; SNF2 family; helicase
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/gene="SPCC1235.04c"
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/gene="SPCC1235.04c"
/note="gtaagt, splice donor sequence"
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/note="gtateg, splice donor sequence"
complement (7185. .11294)
/gene="SPC01235.05c"
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/gene="SPCC1235.04c"
/EC_number="2.7.7.2"
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0%; Score 332.2;
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Saccharomyces servazzii
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AUTHORS
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REFERENCE
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KEYWORDS
SOURCE
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MEDLINE
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JOURNAL
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DRAHRVGOVREVTVIRLITDNTIEFYIQKLANTKLALDMSLSSDGKDREEIGERLVQD
MLDEBNNGNNTKPEITGNESDGEFKVSSNNNSKQTDAEFTNTGVPLEGSQPNSVEXTD
LAADGEKANITKTEMKSETVCGONKELETMKGENVQTDSNAAVPSSKSSTEEPNBSVL
SGHLDLDTEASPVVSTIEKTTKGDVSVTEEQQSANIDGQLEKPEIESSKKPDVLNQVS
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                                                                                              complement (8184. .8435)
/gene="SPCC1235.05c"
/note="Match to helicase_C , Score 83.11"
complement (8721. .9638)
/gene="SPCC1235.05c"
/note="Match to SNF2_N , Score 344.47"
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Pred. No. 3.7e-81;
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Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

8 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This 5TS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis war. lactis, Rluyveromyces maxxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarromia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
GGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACAATGTGTAACGGCTGGAT 1101
                                                                                        2271 GGTGCTAATGCAGTTTTTACCGGTGAAAAAAGCTTACTACTCCTGCTGTTTTCTTGGGAC 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO6K9X 847 bp DNA linear STS 10-JAN-2001 T3 end of clone ATOAA003D06 of library ATOAA from strain CBS 4311 of Saccharomyces servazzii, sequence tagged site.
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Male-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potler, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
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                                                                                                                                                                                                                                    Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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/note="similar to Saccharomyces cerevisiae ORF YGR286c
BIO2 ; blotin synthetase ]"
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                                                                                                                                                                                1102 GAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATGGAGAGTTTCAAATA
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 847)
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/mol_type="genomic DNA"
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/db_txef="taxon:27293"
/clone="ATY0AA003D06"
/clone="ATY0AA003D06"
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1 (bases 1 to 3083)
Holmes, T., Zhang, S., Rich, A., DiPersio, C.Michael. and Lockshin, C. Stable marcoscopic membranes formed by self-assembly of amphiphilic peptides and uses therefore peptides and uses therefore petert. In S955343-A 1 21-SEP-1999;
Location/Qualifiers
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1 (bases 1 to 3083)
Zhang, S., Lockshin, C., Rich, A. and Holmes, T.
                                                                                                                                                                                            Score 328.2; DB 6;
Pred. No. 4.3e-77;
0; Mismatches 163;
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Sequence 1 from patent US 5670483.
I66541

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/organism="unknown"

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Matches 445; Conservative (
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Zhang,S., Lockshin,C., Rich,A. and Holmes,T.
Stable macroscopic membranes formed by self-assembly of amphiphilic
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Patent: US 6548630-A 1 15-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                             613 ACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCAAGAATCTGGAATAAAAGCCTGTACCGGTGGTATTTTGGGTCTCGGTGAAAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTT
                                                                                                                                                                                                                                                       GTCCATGACCTTGGAATGGAGGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCC
                                                                                                                                                                                                                                                                                                          6 GTGAATGATATGGGGCTAGAAACGTGTTACTTTAGGTATGGTTGATCAAGATCAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1024 GTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACA
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1 (bases 1 to 308).
1 that it is 108.
2 inctain, S., Lockshin, C., Herbert, A., Winter, E. and Rich, A.
Zuotin, a putative Z-DNA binding protein in Saccharomyces
                                                                                                                                                                                                       <u>.</u>
ز
                                                                                                                                                     Length 3083;
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                                                                                                                                                                                                  0; Mismatches 163; Indels
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                                                                                                                                                  Score 328.2; DB 6;
Pred. No. 4.3e-77;
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S.cerevisiae ZUO1 gene for zuotin.
X63612. 545839
X63612.1 GI:4836
ZUO1 manno
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93010971
1396572
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Location/Qualifiers
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                                                                                                                                                  Query Match
Best Local Similarity 72.1%;
Matches 445; Conservative
                          1. .3083
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2746. . 2754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERAVSEDPRI KMFKEERKKEKERRKWEREAGRABABABAKAKAEABAKAKABSBAKANA
SAKADKKKAKEAAKAAKKKONKRAIRNSAKEADY FGDADKATTI DEQVGLI VDSLNDEB
LVSTADKI KANAAGAKEVLKESAKTI VDSGKLPSSLLSYFV"
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QFYAFWHRFDSWRTFEFLDEDVPDDSSNRDHKRY1ERKNKAARDKKKTADNARLVKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unnamed protein product; Protein sequence is in conflict with the conceptual translation; ORF within ZUO1"
2 (bases 1 to Jones 2 (bases 1 to Jones 2 (bases 1 to Jones 2 (bases 2 days).

Submitted (20-DEC-1991) S. Zhang, Massachussetts Inst of Submitted (20-DEC-1991) S. Zhang, Massachussetts Inst of State of State of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA Technology, 16-739 Dept of Biology, M I T, Cambridge M 02139, USA Technology, M I T, Cambridge M 02139, USA Technology, M I T, Cambridge M 02139, USA Technology, M 02139, USA Techno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAAACATTCAAAAAC 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAATGATATGGGGCTAGAACGTGTTTACTTTAGGTATGGTTGATCAAGATCAAGCA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1292. .2593
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292. .2593
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Best Local Similarity
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                                                               964 ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAG 1023
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904 AAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC 963
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                                                                                                                                                                                               1084 ATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATG
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September 17, 2005, 14:47:19 ; Search time 731 Seconds (without alignments) 9620.592 Million cell updates/sec
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GenCore version
Copyright (c) 1993 - 2005
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Listing first 45 summaries
                                                                 - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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		Description	Ada09588 Candida u	Adp98553 C. albica	Aba01978 Soybean b	Ade76391 Soybean S	Aat90969 Zuotin ge	Aaz11218 Human zuo	Aad59051 Yeast zuo	Ado04472 Yeast Z-D	Ads15330 Yeast DNA	Aba01974 Maize bio	Ade76383 Corn SID2	Aac48072 Zea mays	Aba01972 Barley bi	Ade76379 Barley SI	Aba01975 Maize bio	Ade76385 Corn SID2	Aba01967 Maize bio	Ade76369 Corn biot	Abz12774 Arabidops	Abv76106 Arabidops
SUMMARIES		di	ADA09588	ADP98553	ABA01978	ADE76391	AAT90969	AAZ11218	AAD59051	AD004472	ADS15330	ABA01974	ADE76383	AAC48072	ABA01972	ADE76379	ABA01975	ADE76385	ABA01967	ADE76369	ABZ12774	ABV76106
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	* Query	Match.	100.0	35.2	29.4	29.4	27.6	27.6	27.6	27.6	27.6	26.2	26.2	26.1	26.1	26.1	26.1	26.1	25.8	25.8	25.6	25.6
		Score	1188	417.6	349.2	349.2	328.2	328.2	328.2	328.2	328.2	311.8	311.8	310.2	310.2	310.2	310.2	310.2	306.6	306.6	304	304
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The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents C. utilis biotin synthase gene.

Adn74336 Thale cre	Aac48445 Arabidops	Aat34580 Biotin sy	Aax01311 A. thalia	Aac33135 Arabidops	Aba01976 Prickly p	Ade76387 Prickly p	Aba01969 Soybean b	Ade76373 Soybean b	Aba01977 Soybean b	Ade76389 Soybean S	Aan91327 E.coli Bi	Adr85519 Asperdill	Adr84932 Aspergill	Adr84345 Aspergill	Aba01973 Maize bio	Ade76381 Corn SID2	Aba01979 Wheat bio	Ade76393 Bread whe	Aca20541 Prokaryot	Ada31411 DNA encod	Aca37222 Prokaryot	Acf68915 Photorhab	Continuation (18 o	Acf65380 Photorhab
12 ADN74336	3 AAC48445	2 AAT34580	2 AAX01311	3 AAC33135	6 ABA01976	10 ADE76387	6 ABA01969	10 ADE76373	6 ABA01977	10 ADE76389	1 AAN91327	13 ADR85519	13 ADR84932	13 ADR84345	6 ABA01973	10 ADE76381	6 ABA01979	10 ADE76393	8 ACA20541	9 ADA31411	8 ACA37222	10 ACF68915	10 ACF67367 17	10 ACF65380
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25.6	25.6	25.6	25.6	25.3	24.9	24.9	24.8	24.8	24.6	24.6	24.6	24.0	24.0	24.0	22.0	22.0	20.5	20.5	20.0	19.9	19.2	19.1	19.1	19.1
304	304	304	304	300.8	295.6	295.6	294.4	294.4	292.8	292.8	292.6	285.6	285.6	285.6	260.8	260.8	243.4	243.4	237.6	236	228.6	226.4	226.4	226.4
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	C 44	c 45

# ALIGNMENTS

Yeast; high biotin-productivity; edible yeast; biotin synthase gene; feed additive; food additive; cosmetic; gene; ds. New integrated plasmid, useful for preparing yeast with high biotin-productivity used as feed additives, food additives or cosmetics. Candida utilis biotin synthase gene. ВЪ. Claim 3; Page 3; 20pp; English. ADA09588 standard; DNA; 1188 02-JAN-2001; 2001US-00752957. 07-OCT-2000; 2000TW-00120972. (first entry) WPI; 2003-567956/53 (SHIU/) SHIUAN D. US2003104584-A1. Pichia jadinii. 06-NOV-2003 05-JUN-2003. ADA09588; Shiuan D; ADA09588

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The invention relates to a novel method for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The method comprises modifying the alleles of a gene in diploid fungal cells method comprises modified. The recombination using a gene disruption cassette and a promoter captacement fragment. The invention further comprises assembling a collection of diploid fungal cells each of which comprises modified alleles of a gene, where the first allele of the gene is modified alleles of a gene, where the first allele of the gene is requence encoding an expressible selectable marker; and the expression of the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene encodes the polypeptide mentioned above; a collection of diploid fungal strains comprising the diploid strains cited above, where substantially all the different genes that encode the above amino acid sequences are modified and are present in different diploid arrains in the collection; a nucleic acid molecule microarray comprising nucleic acid molecules, where each nucleic acid molecule comprising any of the 310 nucleotide sequences listed in the comprising any of the 310 nucleotide sequences listed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Constructing a strain of diploid fungal cells in which both alleles of a gene are modified comprises modifying the alleles of a gene in the fungal cells by recombination using a gene disruption cassette and a promoter
                                                                                                      1081 ACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCA
                            1081 ACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCA
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Candida albicans, where a first allele of a gene comprising any of AD99915.

Candida albicans, where a first allele of a perconduct and accomplishing a compound which modulates the activity of a heterologous promoter; identifying a compound or binding control of a heterologous promoter; identifying a compound or binding confidence or a bloid and albicans, where a first allele of the spolyceptic or preventing or inhibit grown or proliferation of a subject by Candida albicans; or for preventing or inhibit subjects of a negativity or level of a pertapeutic amount of an agent which reduces the activity or level of a pertapeutic amount of an agent which reduces the activity or level of AD99915; methods an intended by a computer and aspect of composition a useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This polynucleotide sequence represents a Candida albicans fungal specific gene of the invention.

NOTE: This sequence was downloaded from an electronic sequence listing specification (ADP98516-ADP98825); identifying a gene that is essential to the survival or growth of a fungus, that contributes to the virulenc provided on the WIPO website. 

Sequence 1125 BP; 362 A; 218 C; 242 G; 303 T; 0 U; 0 Other;

CTGGACCAAAGAAGAAATTAAAGCTATATATGACACACCACTCATGGACTTGATGCACTA 266 TGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACTCTTAT 326 CTGGACCAAAGATGAAATTAGCAAAATTTACAATGCTCCATTGATGGATTTTGATTTTCAA 218 CGCTCAATTGAAACATCGTGAGTACCAAAAACCTGCTGAAGTCCAATTATGTACTCTTGT 278 GAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTA 386 18; 35.2%; Score 417.6; DB 12; Length 67.0%; Pred. No. 6.7e-113; ive 0; Mismatches 299; Indels ; 0 Conservative Similarity 645; 267 Query Match 159 219 207 Local Best Loca Matches g ઠે g 셤 ò

1031 1091 1055 1151 1115 635 863 875 339 TGATACTGGAGTTCAAGCTGAAAAA---CTCGACTTGGATGCTGTGATGGACATTGCTAG 395 563 623 575 743 803 755 911 995 387 CAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAA 996 TITCATGAGTGGGGTCAATGCTATTTTCACCGGTAAGAGAATGTTGACTACAATGTGTAAA 456 AGGAAGAAAGTCTGCCTTAGACAAAATCAGTAAAGTTGTTAAACAAAATCAACGACGAGTT 564 TGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAA 516 GAAGTTGGAAACTTGTGTTACTCTCGGGATGATCAACGAAAAGCAGGCTGAAATTTTAAA AAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAA 684 GGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAAACATTCAAAAAACGTTCAAAGGATC 636 cgrcgrcaccacccgracaracgacgaaagarragaaaccarraaaaacgrccaaaaagc 804 ATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAACAG TICGITITIGIACACITIGIACCAACAACAACAAGAGACCCAGAATCATIGCCAATCAACAA 864 ACTGGTCCCAATCAAGGGCACGCCAATGTATGAA-------GAAGTTAAGAACAA 816 ATTAGTTCCAATCCAGGGTACTCCAATTGTTGAAGTGTTGAAAAATGCACCAAAGGAAAG GCAAGTTGAAGTTGATGATGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAAC 936 ATCCATCATTAGATTGGCCGCCCGGTCGATACACCATGAAGGAACACGAGCAGTTCTTGTG TGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCCAAGAGGACCGTGT GTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTG CTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACACAACAATGTGTAA 1092 CGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGGTCTGAAACCAATGGAGAGTTT Soybean; biotin synthase; biotin biosynthesis; herbicide; plant development; transgenic plant; ss. Soybean biotin synthase coding sequence #4. Location/Qualifiers ABA01978 standard; cDNA; 1659 BP. 06-FEB-2002 (first entry) CA 1153 CA 1117 max. 507 756 1032 1152 624 576 744 912 972 ABA01978; Glycine RESULT 3 ABA01978 Key ద g ð ò 쉽 요 셤 ò ò ò ઠે 셤 ò g ò g ò 유 à 셤 ò 원 ò 원 ò #XSX#XEX#XXXX us-09-752-957f-1.rng

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KINNEY A J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of biotin synthase enzymes from barley, wheat, maize, soybean and the prickly poppy. These sequences can be used to produce transgenic plants which express different levels of the gene, or express it at different times in plant development. They can also be used as a target in the production of herbicides. The present sequence is a soybean biotin synthase CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides, useful as targets for herbicide discovery, and as probes for genetic and physical mapping of genes of which they are par or creating transgenic plants, comprises biotin synthase polypeptides encoding polynucleotides.
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OROZCO E M.
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Matches 595
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                                                                                                  The invention relates to a novel isolated polynucleotide encoding a first polypeptide or a third polypeptide where the first or third polypeptide is a biotin synthase. The methods and compositions of the invention may be useful in plant molecular biology and breeding, particularly in the production of altered levels of biotin synthase in plants and seeds. The polypeptides may be used as a target to facilitate the design and/or identification of inhibitors of these enzymes that may be useful as herbicides. Furthermore, the polypurcleotides may be used as probes for genetically and physically mapping the genes of which they are a part. The current sequence is that of the soybean biotin synthase-related cDNA
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plant molecular biology and plant breeding purposes, particularly in the production of altered levels of biotin synthase in plants and seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 1659;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1659 BP; 496 A; 334 C; 402 G; 427 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 349.2; DB 10; Length
Pred. No. 1.6e-92;
0; Mismatches 378; Indels
                                                            Claim 5; SEQ ID NO 29; 47pp; English.
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60.6%;
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954 PAGGA-----AACAAGAAGGTGGAATTTGAGAATATGTTGAGAATGGTTGCGACGG 1004
                                                                                                                                                                                           rgitaaccacccagccgirgafggggggtcgartccgrcgirifcaacagarggggar 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane-forming peptide; amphiphilic; monovalent metal cation; suture; internal lining; alow-diffusion drug delivery vehicle; erythropoletin; tissue-type plasminogen activator; hemoglobin; insulin; artificial skin; separation matrix; dialysis membranes; filter; collagen; cell migration; shabimer's disease; scrapie infection; therapy; proteolytic digestion; acidic pH resistant; stomach acid; cell adhesion; cell monolayer; zuotin; tissue culture; differentiated cell; stratified cell layer; de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the yeast zuctin gene. Fragments of the encoded protein can be used as the amphibhlic peptides used in the marroscopic membrane (MM) of the invention. The MM is formed by self-assembly of the amphibhlic peptides (see AAM30219-W3033) in an aqueous medium containing monovalent metal cations. The MM are stable in serum, are non-yetotoxic, and are useful in biomaterial applications, such as medical products (e.g. sutures), or internal linings. The MM are useful as slow-diffusion drug delivery vehicles for protein-type drugs, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                   CAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAG
                                                                                                1013 AGGCAGAACAGGTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAA
                                                                                                                               1065 addaAcaacaddacrtrargrrrcarddccdaagccaardccdrrrrcacaddaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membranes formed by self-assembly of amphiphilic peptide(s) - useful bio:material(s), separation matrices, drug delivery vehicles, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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erythropoietin, tissue-type plasminogen activator, synthetic haemoglobin and insulin. They can be used in applications, such as separation matrices (e.g. dialysis membranes). Collagen may be combined with the peptides to produce membranes for use as artificial skin. The MM may be used for making very thin, transparent fabric. Drugs which inhibit the self assembly of the peptides into filaments or filamentous membranes may be useful for treating Alzheimer's disease or scraple infection. As they as receistant to proteolytic digestion and alkaline and acidic, pH (such as remach acid), drug delivery vehicles made of the MM could be taken orally. The charged residues and conformation of the MM promote cell as dhesion and migration. The permeability of the MM also permits diffusion of small molecules, to the underside of cell monolayers, useful for tissue culture of differentiated cells and/or stratified cell layers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Score 328.2; DB 2
Pred. No. 3.8e-86;
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72.1%;
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This sequence encodes the human zuotin (ZUO1) protein. Fragments of the protein can be used in the in vitro method of the invention. The method of the self-assembly of amphiphilic peptides. The peptides are salt-induced to form insoluble and protease-resistant protein filaments with a beta-sheet secondary structure. The membranes may be may be useful in a wide variety of medical, research, industrial and blomaterial applications such as slow-diffusion drug delivery systems, artificial skin and separation matrices. The membranes may be used to support in vitro cell attachment and growth and for supporting artificial tissue (e.g. for in circase minglants). They are particularly useful as experimental or vivo use as implants). They are particularly useful as experimental crowing artificial tissue (e.g. for in disease modelling experiments and scrapic infection and so may be used in disease processes. Additionally, they may be used in this way to study liver cirrhosis, kidney amyloidosis and other protein conformational diseases. The membrane in the membrane/cell mixture produced in the method: (i) supports cellular attachment and growth; (ii) self-assembles to form large, macroscopic membranes that are insoluble conditional adueous solutions, serum and ethanol; (ii) is and stable in a queous solutions, serum and ethanol; (iii) is a highly resistant to heat, alkaline/acidic phs. chemical denaturants and conformational and processing serum and ethanol; (ii) may conformational maked eye if qwed but is otherwise transparent; (v) is conformational maked eye if qwed but is otherwise transparent; (v) is conformational maked eye if qwed but is otherwise transparent; (v) is conformational maked eye if qwed but is otherwise transparent, (v) is which the setulation of the protein of the pr
                                                                  Membrane forming peptide; cell culturing; macroscopic membrane; amphiphilic peptide; alow-diffusion drug delivery system; cell growth; artificial tissue; separation matrix; artificial tissue; scrapie infection, Alzheimer's disease; liver cirrhosis; kidney amyloidosis; protein conformational disease; human; zuotin; ZUO1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         form thin, permeable, high density sheets or fibril like structures with simple structures, high tensile strength and a porous structure; (vii) may be metabolised by humans and animals; (viii) is inexpensive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cultures utilizing stable macroscopic membranes formed by the self-assembly of amphiphilic peptides.
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llarity 72.1%; Pred. No. 3.8e-86;
Conservative 0; Mismatches 163;
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1292. .2593
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                      Human zuotin coding sequence.
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GTGAATGATATGGGGCTAGAAACGTGTTACTTTAGGTATGGTTGATCAAGATCAAGCA 65

09-NOV-1999 (first entry)

AAZ11218;

RESULT 6
AAZ11218
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                        513 ACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAA
                                                                          CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAAC
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The invention relates to a macroscopic membrane formed by self-assembly of amphiphilic peptides in an aqueous solution containing monovalent metal cations. The peptides have alternating Mydrophobic and hydrophilic amino acids and are complementary and structurally compatible. The membranes are useful as biomaterial for medical products (e.g. sutures, artificial skin, internal linings), as vehicles for slow-diffusion drug delivery (preferably for protein type drugs e.g. erythropoietin, tissue type plasminogen activator, synthetic haemoglobin and insulin), as separation matrices (e.g. dialysis membranes, chromatography columns, filters for the removal of viruses and other microscopic contaminants), for other uses requiring permeable and water-insoluble material (e.g. for culturing cell monolayers including differentiated cells and/or stratified cell layers), for the preparation of very thin and transparent fabric and as a model system for investigating the properties of biological protein structures and providing insights into the pathology and proteins compassing structures (e.g. Alzheimer's disease, scrapie infection and in origin of life studies related to cell membranes and cellular comparatentalisation). The present sequence is yeast zuctin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macroscopic membrane useful in biomaterial applications e.g. sutures is formed by self-assembly of amphiphilic peptides in an aqueous solution containing monovalent metal cations.
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                                     "Yeast zuotin protein"
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P-PSDB; AAE38829.
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Best Local Similarity
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30-NOV-1994;
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(HOLM/) HOLMES T.
(ZHAN/) ZHANG S.
(RICH/) RICH A.
(DIPE/) DIPERSIO C M.
(LOCK/) LOCKSHIN C.
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P-PSDB; ADO04473.
                                                                                                                                              Holmes T, Zhang S,
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22-AUG-1994;
26-MAR-1997;
                        06-MAY-2004
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                                                                   AAGAGTAAAAAGTTGCAATTCGACGAATTTTGAGAACCATTGCCACAGGGAGAATAGTT 425
                                                                                                    Argechandecearranadaerrecegeregregrearaneareangandageda 485
GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCCTGAGTCCCTA 305
                                                                                                                                                                                                                                                                                                                        Macroscopic membrane; cell growth; EAK16; Z-DNA binding protein; zuotin; medical product; suture; artificial skin; internal lining; slow-diffusion drug delivery system; protein-type drug; erythropoietin; haemoglobin; insulin; cell adhesion; cell migration; Alzheimer's disease;
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                                                  AAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC
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/note= "7 AT repeats"
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/note= "8 AT repeats"
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701. .714
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/rpt_type= TANDEM
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The invention relates to a method for in vitro cell culture which involves adding a macroscopic membrane that is formed by self-assembly of amphiphilic peptide in an aqueous solution containing monovalent metal cations to a cell culture medium comprising cells, thus forming a membrane/culture mixture, maintaining the mixture under conditions a sufficient for cell growth. The invention also relates to EAK16 peptide certical for cell growth. The invention also relates to EAK16 peptide into the macroscopic membranes are useful in biomaterial applications such as medical products (e.g., sutures), artificial skin or internal into the macroscopic membranes are useful in biomaterial applications such as medical products (e.g., sutures), artificial skin or internal lings, slow-diffusion drug delivery systems supports for in vivo use, as slow-diffusion drug delivery thicle for delivering protein-type drugs conductive biopolymer for culturing cell monolayers, for promoting cell adhesion and migration, useful as experimental models for Alzheimer's disease and scrapic infection. The present sequence is yeast zuotin DNA. This sequence is useful as the invention.
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94US-00293284.
97US-00824515.
17-MAR-2003; 2003US-00390472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell culture; macroscopic membrane; amphiphilic peptide; biomaterial; slow-diffuaion drug delivery system; artificial skin; separation matrix; Alzheimer's disease; scrapie, liver cirrhosis; kidney amyloidosis; protein conformational disease; yeast; DNA binding protein; zuotin; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of culturing (M1) cells, in vitro. The cell culture involves adding a macroscopic membrane which is formed by
                             AAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC
                                                                                                            <u> aagagraaaagrigcaaricgacgaaaririrgagaaccarigccacagcgagaaragrr</u>
                                                                                                                                                 ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAG
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monovalent metal cations, where the peptides have alternating hydrophobic and hydrophilic anino acids and are complementary and structurally compatible, to a cell culture medium complementary and structurally compatible, to a cell culture medium comprising cells, thus forming a membrane/culture mixture, and maintaining the mixture under conditions is sufficient for cell growth. (MI) is useful for culturing a macroscopic membrane utilised in biomaterial applications e.g., slow-diffusion drug delivery systems, artificial skin or separation matrices, or as delivery systems, artificial skin or separation matrices, or as caperimental models for Alzheimer's disease and scrapic infection e.g., liver cirrhosis, kidney amyloidosis, or other protein conformational diseases. (MI) enables in vitro culturing of macroscopic membrane that is stable in aqueous solution, serum and ethanol, highly resistant to heat, alkaline and acidic ph, chemical denaturants and proteolytic diseasin, and is non-cycloxic. This sequence encodes yeast DNA binding protein contour amphiphilic peptides capable of forming membrane can be
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(MIAO/) MIAO G.
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                                                                                                                                                                                                                                                    Maize; biotin synthase; biotin biosynthesis; herbicide; plant development; clone cholc.pk009.j14; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1515 BP; 467 A; 368 C; 368 G; 312 T; 0 U; 0 Other;
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Pred. No. 2e-81;
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/product= "biotin synthase"
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                                                                                                                                   synthase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cocation/Qualifiers
131. .1264
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Fig 2; 46pp; English.
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Best Local Similarity 59.1%;
Matches 557; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2000; 2000US-00740288
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                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINNEY A J.
MIAO G.
OROZCO E M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-040723/05
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                                                                                                                                         Maize biotin
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                  06-FEB-2002
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(KINN/) H
(MIAO/) N
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                                                                                                                                            GGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACAATGTGTAACGGCTGGGAT 1101
 851 GTAGGGTTGTTGCATACCCTAGCTACCTTGCCTACACACCCCAGAGAGGGGTTCCTATTAAT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                        911 GCATTGGTTGCTGTAAAAGGCACACCTCTTGAGG------ACCAGAAGCCTGTAGAG
                                                                                                                                                                                                                   AGGCTTTCAGCAGGCCGAGTACGGTTCTCGATGCCAGAACAAGCGCTGTGCTTCCTCGCT
                                     GTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC
                                                                                                                                                                                 AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT
                                                                                                                                                                                                                                                                                                                            GAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATGG 1144
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9905-0123180P-
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9905-0125788P-
9905-0125785P-
9905-012674P-
9905-0128234P-
9905-0128234P-
9905-0128234P-
9905-013091P-
9905-0130510P-
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99US-0134370P.
99US-0134768P.
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05-MAR-1999
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30-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610
                                                                                                                                                                                                                                The invention relates to a novel isolated polynucleotide encoding a first polypeptide or a third polypeptide where the first or third polypeptide is a biotin synthase. The methods and compositions of the invention may be useful in plant molecular biology and breading, particularly in the production of altered levels of biotin synthase in plants and seeds. The polypeptides may be used as a target to facilitate the design and/or identification of inhibitors of these enzymes that may be useful as herbicides. Furthermore, the polypucleotides may be used as probes for genetically and physically mapping the genes of which they are a part. The current sequence is that of the corn biotin synthase-related CDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAAAGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGAG 501
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                                                                                                                       New isolated polynucleotide encoding plant biotin synthase, useful in plant molecular biology and plant breeding purposes, particularly in the production of altered levels of biotin synthase in plants and seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACACCTGGACCAAAGAAATTAAAGCTATATATGACACACCACTCATGGACTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1515 BP; 467 A; 368 C; 368 G; 312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 311.8; DB 10; Length
Pred. No. 2e-81;
0; Mismatches 377; Indels
                                     Orozco
                                                                                                                                                                                              Claim 5; SEQ ID NO 21; 47pp; English.
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59.1%;
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nes 557; Conservative
                                     Kinney AJ,
                                                                       2003-831831/77.
(OROZ/) OROZCO E M.
                                                                                      P-PSDB; ADE76384.
                                   Allen SM,
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99US-0145951P. 99US-0146386P. 99US-0146389P. 99US-0147038P. 99US-0147038P. 99US-0147192P. 99US-0147192P. 99US-0147192P. 99US-0147192P. 99US-0147192P.	900S-0148171F 900S-0148119F 900S-0148684P 900S-0148684P 900S-0149368P 900S-0149375P 900S-0149426P 900S-0149723P 900S-0149723P 900S-0149723P 900S-0149723P 900S-0149723P 900S-0150566P 900S-0150864P 900S-0150864P	99US-0151080P. 99US-01514303P. 99US-01514303P. 99US-0152363P. 99US-0152363P. 99US-01530703P. 99US-01530703P. 99US-0154018P. 99US-0154018P. 99US-0155408P. 99US-0155408P. 99US-015548P. 99US-015548P. 99US-015548P. 99US-015548P. 99US-015548P.	99US-0158232P. 99US-015234P. 99US-0152294P. 99US-0152295P. 99US-0153295P. 99US-0153310P. 99US-0153310P. 99US-0153310P. 99US-0153310P. 99US-015634P. 99US-0160764P. 99US-0160764P. 99US-0160764P. 99US-0160764P. 99US-0160764P. 99US-0160764P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P. 99US-0160768P.
28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 09-AUG-1999;	10-AUG-1999; 11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 16-AUG-1999; 16-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999;	27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 07-SEP-1999; 10-SEP-1999; 11-SEP-1999; 16-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 24-SEP-1999; 04-OCT-1999; 05-OCT-1999; 07-OCT-1999;	00-0CT-1999; 13-0CT-1999; 13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 12-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 25-0CT-1999; 25-0CT-1999;
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99US-0134941P. 99US-0135124P. 99US-0135523P. 99US-0136629P. 99US-0136722P. 99US-0137522P. 99US-0137528P. 99US-0137528P. 99US-0137528P.	9905 - 013945 P.	99US-0139817P. 99US-0140353P. 99US-0140353P. 99US-0140354P. 99US-0140823P. 99US-0140823P. 99US-0141842P. 99US-0141842P. 99US-0142154P. 99US-0142390P. 99US-0142390P. 99US-0142390P. 99US-0142390P. 99US-0142390P. 99US-0142390P. 99US-0142977P.	99US-0144086P 99US-0144331P 99US-0144331P 99US-0144331P 99US-0144331P 99US-0144331P 99US-0144332P 99US-0144632P 99US-0144632P 99US-0144814P 99US-014508P 99US-014508P 99US-014508P 99US-014508P 99US-014508P 99US-014518P 99US-014518P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P 99US-0145218P
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1072 GCGGACCAGGCGATGTTCAAGATCCTTGGCCTGATCCCCAAGG 1114
                                                                                                                          Barley biotin synthase coding sequence
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                                                                                                                                                                                                        Location/Qualifiers
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/*tag= a
/product= "biotin
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                                                       ABA01972 standard; cDNA; 1396
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ilarity 59.0%;
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KINNEY A J.
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P-PSDB; AAM51979.
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es 556; Conserv
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                                                                                                                                               biotin
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                                                                                                                                                                       321
                                                                                                                                                                                            241 TTTCACGGGGCTCAGGTCCACAGAAATGTCCATAAATTCAGAGAAGTGCAGCAATGCACA 300
                                                                                                                                                                                                                                         CTTCTTTCAATCAAGACTGGTGGATGCAGTGAAGATTGTTCTTACTGTCCTCAGTCATCA 360
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                                                                                                                           202 AACACCTGGACCAAAGAAAATTAAAGCTATATATGACACACCACTCATGGACTTGATG
                                                                                                                                               CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                                                                                                CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT
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                                                                                                    Indels
                                                                              DB 3;
                                                                                                    377;
                                                                                         5.4e-81;
                                                                                                  , 4; Mismatches
                                                                              26.1%; Score 310.2; 58.6%; Pred. No. 5.4
                                99US-0161992P.
99US-0161993P.
99US-0162142P.
          99US-0161361P
99US-0161920P
                                                                                                    Conservative
                                                                                         Similarity
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
                                 28-OCT-1999;
28-OCT-1999;
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v polypeptides, useful as targets for herbicide discovery, and as
bbes for genetic and physical mapping of genes of which they are, part,
creating transgenic plants, comprises biotin synthase polypeptides and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 AACACCTGGACCAAAGAAATTAAAGCTATATATGACACACCACCACGACTTGATG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT
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                                                                              seedling;
                                                                              Barley, biotin synthase, biotin biosynthesis, herbicide, seedli
plant development; clone bshl.pk0005.d10; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Pred. No. 5.6e-81;
0; Mismatches 378;
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/note= "the sequence has no
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202 AACACCTGGACCAAAGAAGAATTAAAGCTATATATGACACACCACTCATGGACTTGATG 261
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                                                                                                                  07-MAY-2003; 2003US-00431544
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Matches 556; Conservative
                                                                                                                                                                                                     21-DEC-1999;
19-DEC-2000;
                                       09-OCT-2003
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                                                                          chrcirrcaahaaagachganggangcagagaaarrgircanakugcagagagtutua 392
CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAG 381
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plant; breeding; seed; herbicide; ss; gene; barley;
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                                                     biotin synthase cDNA
             ВР
             standard; cDNA; 1396
                                       (first entry
                                                                   synthase;
                                                                                       Hordeum vulgare.
                                                                                                     US2003192073-A1
                                                     SID18
                                        29-JAN-2004
             ADE76379
                          ADE76379
                                                     Barley
                                                                  biotin
                                                                          SID18.
RESULT 14
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The invention relates to a novel isolated polynucleotide encoding a first polypeptide or a third polypeptide where the first or third polypeptide is a biotin synthase. The methods and compositions of the invention may be useful in plant molecular biology and breeding, particularly in the production of altered levels of biotin synthase in plants and seeds. The polypeptides may be used as a target to facilitate the design and/or identification of inhibitors of these enzymes that may be useful as herbicides. Furthermore, the polynucleotides may be used as probes for genetically and physically mapping the genes of which they are a part. The current sequence is that of the barley biotin synthase-related cDNA
                                                                                                                                                                                                                                                                                                                 New isolated polynuclectide encoding plant biotin synthase, useful in plant molecular biology and plant breeding purposes, particularly in production of altered levels of biotin synthase in plants and seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1396 BP; 387 A; 351 C; 356 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 310.2; DB 10;
Pred. No. 5.6e-81;
0; Mismatches 378;
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                                                                                                                                                                    Orozco
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59.0%;
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                                                                                                                                                                    SM, Kinney AJ,
ALLEN S M.
KINNEY A J.
MIAO G.
                                                                                                                                                                                                                               WPI; 2003-831831/77.
P-PSDB; ADE76380.
                                                                                                     OROZCO B M.
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The present invention provides the protein and coding sequences of biotin synthase enzymes from barley, wheat, maize, soybean and the prickly poppy. These sequences can be used to produce transgenic plants which express different levels of the gene, or express it at different times in plant development. They can also be used as a target in the production of herbicides. The present sequence is a maize biotin synthase cDNA obtained from clone cca.pk0012.g11:fis
probes for genetic and physical mapping of genes of which they are part, or creating transgenic plants, comprises biotin synthase polypeptides and encoding polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     982 AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT 1041
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                                                                                          Claim 5; Page 29-30; 46pp; English.
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                                                                  AACATTATTTTCTACAAGATCGTATGATGATTACAGACTCTTCAGCATGTCGAA
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                            <u>AAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGA</u>
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
               Copyright
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OM nucleic - nucleic search, using sw model

September 17, 2005, 16:11:49 ; Search time 236 Seconds Run on:

(without alignments)
8236.851 Million cell updates/sec

Perfect score:

US-09-752-957F-1 1188 1 atgtcgtttatattgactgc.....aggttgcattcggtgcttga 1188 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 seqs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2 6/ptodata/1/ina/5A COMB.seq:\*
2: /cgn2 6/ptodata/1/ina/5B\_COMB.seq:\*
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5: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:\*
6: /cgn2 6/ptodata/1/ina/PcTUS COMB.seq:\* Issued Patents NA:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	ce 444	US-08-346-849-1 Sequence 1, Appli	'n	Sequence 1,	ų	13,	3 Sequence 13,	2698,	91	9 Seguence 709, 1	۲,	<u>ښ</u>	1 Sequence 1,	Sequence 1,	$\sim$	28 Sequence 28,	1, 1	Sequence 117		334	Sequence 7,	7,	'n	US-08-411-768B-6 Sequence 6, Appli	25,	70,	•
S	ID	0S-09	US-08	US-08	US-08	0S-08	US-08	US-08	0S-09	US-09	0S-09	US-0	US-0	ns-0	0-SD	0S-09	0S-09	US-09	US-09	0S-09	.60-SD	US-08	US-08	US-08	US-08	0S-09	0S-09	
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	Sequence 3895, April April 2895, April 289	Sequence 2561, Apr Sequence 3934, Apr	Sequence 14, Appl Sequence 1, Appl
US-09-489-039A-5954 US-09-540-236-1834 US-09-540-236-1834 US-08-781-986A-338 US-08-935-263-7 US-09-534-185-7 US-09-534-18-7 US-09-633-927-1 US-09-134-001C-634 US-09-134-001C-634	US-09-710-279-3895	US-09-710-279-2561 US-09-710-279-3934	US-08-232-463-14 US-08-916-421B-1
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## ALIGNMENTS

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Sequence 4445, Application US/09248796A

Batent No. 6747137

GENERAL INFORMATION:
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GENERAL TITLE OF INVENTION:
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
FROR RILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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Pred. No. 3.4e-122;
0; Mismatches 301;
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Best Local Similarity 66.8%;
Matches 643; Conservative
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Pred. No. 2.9e-94;
0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1292..2590
OTHER INFORMATION: /product= "zuotin"
                                                                                                             NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERNICE/DOCKET NUMBER: MIT-6008
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3083 base pairs
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326.
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1144 GAGAGTTTCAAATACAA 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%;
                                                                                                                                                                                                                                                                                                                 LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 72.1
Matches 445; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                                                                        TICGITITITIGIACACTITIGICCAACATGAGTCCCCAGGAATCATTGCCAATCAACAG 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGT------TAAGAACAA 911
                                            654 GAAGTIGGAAACTIGIGITACTCICGGGAIGATCAACGAAAAGCAGGCIGAAATTTIAAA 713
                                                                                                                                                                                              GGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGATC 743
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564 TGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAA
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APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Taxale MACROSCOPIC MEMBRANES FORI
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEP
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/08346849; Patent No. 5670483; GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, Shuguang
Lockshin, Curtis
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Massachusetts
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ZIP: 02173-4799
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| CA 1255
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US-08-346-849-1
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793 GAGGACCGIGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTTT
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REGISTRATION NUMBER: 2,592
REFERENCE/DOCKET NUMBER: MIT-6008FB
TELECOMUNICATION INFORMATION:
TELECHONE: (781) 861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08898300
; Patent No. 6548630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCATTTAAGTACGA 622
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                                                                                                      APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Lockehio, C. Michael
APPLICANT: DiPersio, C. Michael
APPLICANT: DiPersio, S. Michael
APPLICANT: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TOWNER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 3083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 27.6%; Score 328.2; DB 2; Length Best Local Similarity 72.1%; Pred. No. 2.9e-94; Matches 445; Conservative 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                    E: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FLING DATE: 22-AUG-1994
CLASSIFICATION 1435
PRIOR APPLICATION DATE: 07/973,326
ATOMOR APPLICATION NUMBER: 07/973,326
ATOMORY/AGENT INFORMATION:
NAME: BLOOK, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1292..2590
OTHER INFORMATION: /product= "zuotin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MIT-6008A TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           ; Sequence 1, Application US/08293284A; Patent No. 5955343; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 861-624
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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1084 ATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATG 1143
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                                                                                                                                                                                                                                                                                                                                                                                      964 ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCCAGAACAG 1023
246 gacgaccararaggarricarcracacarrarccaarargrerccrcarccragactra
                                                                                                                                                       306 cchartharhachchachrachhanchanchartachanagarthachanach 365
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                                                                           853 CCAATCAACAGACTGGTCCCAATCAAGGCCACGCCAATGTATGAAGAAGTT-----
                                                                                                                                                                                                                                   904 AAGAACAAGCAAGTIGAAGTIGATGAGATIGICAGAACCATIGCTACTGCAAGATIGGIC
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SELF-ASSEMBLY OF AMPHIPHILIC PRPTIDES AND USES
THEREFOR
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Two Militia Drive
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: Patent For DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,300
FILING DATE: 22 JULY 1997
CLASSIFICATION NUMBER: 08/346,849
FILING DATE: 30 NOVENBER 1994
PRIOR APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATPONEY/AGENT INFORMATION:
AAPPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATMONEY/AGENT INFORMATION:
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CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAAC 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.6%; Score 328.2; DB 4; Length 72.1%; Pred. No. 2.9e-94; tive 0; Mismatches 163; Indels
                                                                                                                                                                    ZIP: 021/4/99

COMPUTER 1021/4/99

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,513
FILING DATE: March 26, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/293,284
FILING DATE: August 22, 1998
PRIOR APPLICATION NUMBER: 09/293,326
FILING DATE: August 22, 1998
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: BLOCK, DAVIG E.
REGISTRATION NUMBER: MIT-6008A2
REFERENCE/DOCKET NUMBER: MIT-6008A2
REFERENCE/DOCKET NUMBER: MIT-6008A2
                                         BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1292..2590
; OTHER INFORMATION: /product= "zuotin"
US-08-824-513-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781) 861-6240
TELEPAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                               Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3083 base pairs
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Best Local Similarity 72.1
Matches 445; Conservative
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON,
STREET: Two Militia D
                                                                                          Lexington
Massachusetts
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STRANDEDNESS: double
NUMBER OF SEQUENCES:
                                                                                        CITY: Lexington
STATE: Massachuse
COUNTRY: U.S.A.
ZIP: 02173-4799
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Rich, Alexander
DiPersio, C. Michael
Lockshin, Curtis
VENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
VENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
VENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                            DB 4; Length 3083;
                                                                                                                                                                                                                                                         27.6%; Score 328.2; DB 4; Length 72.1%; Pred. No. 2.9e-94; ive 0; Mismatches 163; Indels
                                                                                                                                                            COCATION: 1292..2590
CTHER INFORMATION: /product= "zuotin"
US-08-898-300-1
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Patent No. 6800481
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexader
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSC
TITLE OF INVENTION: THEREFOR
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                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
3083 base pairs
                                                                                                                                                                                                                                                                                                          Matches 445; Conservative
                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                   FEATURE:
NAME/KEY:
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                                                                                                CTIATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAG
                                                                                                                                                                                                                                                                                                                                  ATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic Plants Having Increased Biotin Content
                    CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                         382 CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCA
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STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08846338;
Patent No. 5869719;
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Transgenic Pl
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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US-08-846-338-13
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                                                                                                                1024 GTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACA 1083
                                                              486 Trrereretrargecaeerreraacagraretreaceeraagaaargereaceaca 545
                                                                                                                                                                                                                     36 AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGCGAGAATAGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AACGATTGGAGTAGAGATGAATCAAGTCTGTTTATGATTCTCCTCTTTGACCTCCTC 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enhanced Biotin Biosynthesis in Plant Tissue
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; OTHER INFORMATION: /product= "Arabidopsis BioB enzyme"
US-08-401-068-13
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Pred. No. 1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08401068
Patent No. 5859335
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Enhanced Biotin Bi
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/351,970
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Blmer, James Scott
REGISTATION NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-51-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,068 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                           GAGGCATTTAAGTACGA 622
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58.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
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Best Local Similarity
Matches 551; Conserv
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HYPOTHETICAL:
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US-08-401-068-13
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Sequence 2699, Application US/09328352

Requence 6562958

GREERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GT-99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 2698

LENGTH: 1017
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742 TCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGT 801
                                                                                                                                                                                                                                  854 GCTCTACTTGCAGTGAAAGGCACTCCTTGAAG-----ACCAGAAGCCAGTTGAG 904
                                                                                                                                                                                                                                                                                   GTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC 981
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                                                                                        GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTTCCAATCAAC
                                                                                                                                    794 ATAGGTTTATTACACACGCTGGCAACACTTCCTTCTCACCCTGAGAGTGTTCCCATTAAT
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                                              734 GCTGGAATCAACGTTTGTTCAGGAGAATCATAGGGCTTGGTGAGGCAGGAGAAGACAAA
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19.9%; Score 236; DB 4; Length 10
Best Local Similarity 54.7%; Pred. No. 5.9e-65;
Matches 520; Conservative 0; Mismatches 415; Indels
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US-09-328-352-2698
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US-09-328-352-2698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 CICCICICCATAAAGACIGGIGGIGGIAGIGAAGACIGIICAIATIGICCICAGICITICG 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAAAGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGAG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTAAGGAAAGGAAAGAAGCTGGGAGCACACGTTTTTGCATGGGTGCTGCTTGGCAGAT 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 TTCCATGGAGCTCAGGTTCATAGACATGTTCATAACTTCAGGGAGGTACAACAATGTACC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGAC 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Argeggarggaagrirgcrgcaccrraggcargaricagaaacaacaagcacragagcra 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGTCATCACTACTAGAAGTTATGACGATCGCCTTGAAACTCTTAGCCATGTTCGTGAT 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 59..1192
; OTHER INFORMATION: /product= "Arabidopsis biotin synthase enzyme"
US-08-846-338-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 304, DB 2, Length 1351;
Pred. No. 1e-86;
0, Mismatches 380; Indels
                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/646,338
                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.6%;
                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 58.6
Matches 551; Conservative
                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
         Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CI
                                                   USA
                                                                                                                                                                                                                                                               FILING DATE:
                                                                       10591
                                                   COUNTRY:
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GGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTTG 1046
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Patent No. 6833447

GENERAL INPORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Waspard, Roger C.
TILLE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof;
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540
TGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACTCTTAT
                                                                                                                                                                                                                                CAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAA
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                                                                                                              GAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTA
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                                                     GGCCCAGACGGTCCACCGGGCCGTGTTCGTGGACAACAAGGTCCAGCTCTGTTCGCTGCT
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US-09-902-540-709/c
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                                                                                                                                                                       GCCACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAG 669
                                                                                                                                                                                                                                                                                      GAACACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAA 729
                                                                                                                                                                                                                                                                                                                             CAAGAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCT 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910 AAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCA 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - AAAAACTAGATGTTATTGAATGGATTCGTACTATTGCGGTAGCGCAGGTATCATTATGCCG 792
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                                                                                                              GCAGAACGCCTAAAAGATGCCGGTTTAGACTATTACAACCATAACCTTGATACTTCTCGC 501
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GCTTGGCG-----CAACCCTCATGAGCGCGATATGCCTTATGTTTTAGAAATGGTACGT 381
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                                                        GCTGTCCATGACCTTGGAATGGAGGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAA
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Patent No. 6813447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Seq:

FILE REPERENCE: 38-10(15849)B

CURRENT APPLICATION UNDRER: US/09/902,540
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PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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ORGANISM: Myxococcus xanthus
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SEQ ID NO 7391
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Matches 512; Conservative
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US-09-902-540-7391
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US-09-557-884-1
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                                                                                                                                                                                                Score 230.4; DB 4; Length Pred. No. 9.1e-63; O; Mismatches 416; Indels
CURRENT FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 16825 SEQ ID NO 709
                                                                                                                                                                                                19.4%;
ilarity 54.5%;
Conservative
                                                                                                                         ; TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-709
                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches 512;
                                                                                                       4183
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1107 TARAGCCATGTTGGCTRAATGGGGTCTGAAACCAATGGAG 1146
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                                                                                                                                                                                  Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF INVENTION: The Themophilus influenzae
Thereof, and Uses Thereof
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llarity 54.3%; Pred. No. 4.7e-55;
Conservative 0; Mismatches 404;
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3 1/2 inch diskette COMPUTER: Dell Pentium
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FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
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REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1830121 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: doubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
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1085788 AAAATCAGCAGTTATTAGATGTTGATGAGATCGTCGCTAAAGCAAAAATTGCGAAAGCAC 1085847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1086081 Gririgaricarcerragcacerraggaaaacreecaaageresarraaaacreerr 1086140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1086141 GTGGTGGCATTGTAGGGATGAATGAAACTCGCAAAGAACGGGCTGGATTAATCGCGAGCC 1086200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1085668 Arcerakecarrrraarcerececearreagriarecacerraarerrareaaaacee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTACAACACTGGTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Gaps
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54.3%; Pred. No. 4.7e-55;
tive 0; Mismatches 404;
                       APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                       NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
PILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1830121 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 301-610-5790
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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Matches 500; Conservative
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1085848 GTGGTGCAGGGCGTTTCTGTATGGGGGCTGCTTGGCGAGGCCCTAAGCCAA-----AAG 1085901
                                                                                                                                           1085902 ATATTGAGAAAGTCACAGAAATTATTAAAGCCGTGAATCACTTGGTTTAGAAACTTGCG 1085961
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Thereof, and Uses Thereof
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                                                                           ACTIGAAGAAAATCAAAGAGAIGAICACIGCIGICCAIGACCIIGGAAATGGAGAGTIGIG
                                                                                                                                                                                                                               TCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGG
                                                                                                                                                                                                                                                                                               1085962 GTACCTTTGGTTTATTGCAAGACGGTATGGCGGAAGATTTAAAAGAAGCTGGATTAGATT
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J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3 1/2 inch diskette COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS v6.22 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1086492 CAAAATTAGATTTAGAGCCA 1086511
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Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAAATGGGGTCTGAAACCA 1140
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COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
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US-09-643-990A-1
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NAME/KEY: misc feature
LOCATION: (330001). (345000)
OTHER INFORMATION: n=a or or g or t
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LOCATION: (345001). (360000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (360001). (375000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (49501)..(510000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (270001)..(285000)
JTHER INFORMATION: n=a or c or g or t
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LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (285001)..(300000)
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OCATION: (37501)..(39000)
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OCATION: (390001)..(405000)
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LOCATION: (450001)..(465000)
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LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (480001)..(495000)
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THER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or
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LOCATION: (25501)..(270000)
OTHER INFORMATION: n=a or c or g
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LCCATION: (22501)..(240000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
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THER INFORMATION: n=a or c or
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LCCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or
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OCATION: (405001)..(420000)
THER INFORMATION: n=a or c or
                          INFORMATION: n=a or c or
                                                                  LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or
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Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, F
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION WUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                 1086432 ATGGCGATAAATTACTTGTTACAGATAATCCAGAAGAAGAGGTGGCGATCAGTTATTGATGG 1086491
                                               1086261 GTACGCCGTTAGCCGATGCGG-----AGGAATTAGATTGGACGGAGTTTGTGCGAA 1086311
                                                                                                                                    1086372 GIGGIATGACTGAAGAAATGCAAGCGATGTTTTTATGGCGGGTGCAAATTCTATTTTT 1086431
                                                                                                  941 CCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGAT 1000
                                                                                                                                                                                                    1001 ATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCA 1060
                                                                                                                                                                                                                                                                                                    1061 CAGGTAAGAAATGCTCACAACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGG 1120
881 GCACGCCAATGTATGAAGAAGTTAAGAACAAGCAAGTTGAAGTTGATGATGTCAGAA 940
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LOCATION: (90001). (105000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (120001)..(135000)
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NAME/KEY: misc_feature
LOCATION: (1). (15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (15001). (30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (30001). (45000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (135001)...(150000)
OTHER INPORMATION: n=a or c or g or t.
NAME/KEY: misc feature
LOCATION: (150001)...(165000)
OTHER INFORMATION: n=a or c or g or t.
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LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or
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ORGANISM: Chlamydia pneumoniae
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LOCATION: (75001)..(900
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US-09-198-452A-1/c
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LOCATION: (88501)..(900000)
JTHER INFORMATION: n=a or c or g or t
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LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (585001). (600000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (810001)..(825000)
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COCATION: (645001)..(660000)
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THER INFORMATION: n=a or c or g or AMB/KEY: misc_feature
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LOCATION: (55501)..(570000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (570001)..(585000)
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COCATION: (73501)..(75000)
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INFORMATION: n=a or c or g
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1208824 CCTGGTCATTAGAAGACATCCGCGAAATTTATCACACTCCCGTATTTGAGCTGATTCACA 1208765 1208764 AAGCCAATGCCATATTGCGTAGTAATTTCCTCCATTCAGAACTGCAGACTTGCTATCTGA 1208705 1208704 TTTCGATTAAAACTGGTGGATGCGTTGAAGATTGCGCCTACTGTGCCCAATCTTCCCGCT 1208645 1208585 1208584 AACGTGCTGTAGAGCTAGGCGCCACTGTGTGTTTTGGGGCTGCCTGGCGCATGCTA 1208525 1208524 AGG---ACGATCGATACTTTGATAGAGTCCTCGCTATGGTGAAAAGTATCACAGATCTCG 1208468 1208467 GAGCCGAGGTTTGTTGCTTTTAGGCATGCTCTCCGAAGAGCAAGCTAAAAAACTGTATG 1208408 1208407 ATGCAGGACTTTATGCCTACAATCATAATTTAGACTCTTCTTCCGGAATTCTATGAAACTA 1208348 1208287 GCATTAGTACATGCTGCGGTGGTATTGTAGGTATGGGAGAATCTGAAGAAGACCGTATAA 1208228 1208227 agcritcricargricricaacaacaagagarcararcccagaarccgraccrgraarriac 1208168 1208167 irregecegarreacegecaceerriecaagaceacecrecea-----rirerrier 1208117 1208116 GGGAAGTCTTGCGAACCATAGCAACGGCACGGGTTGTTTTCCCCAGATCCATGGTACGAC 1208057 1207996 CCAACTCCATATTCTATGGAGATAAACTGTTGACTGTAGAAAACAATGATATAGATGAAG 1207937 1208056 TTGCTGCAGGACGCGCTTTCCTCACAGTAGAACAACAAACCTTATGTTTTCTAGCCGGTG 1207997 1045 865 GAATGGAGAGTTGTGTCTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAA 625 206 CCTGGACCAAAGAAGAATTAAAGCTATATATGACACCACCACCATGGACTTGATGCACT 266 ATGCTCAGGTGCAACACAGAAGGTTCCAACATCCTTCAGAGGTTCAATTGTGCACTCTTA TGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTT 386 ACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAA 446 AGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGATGA AAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGACCTTG GTGCTGGGTTGACGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAAGG GATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGTGTAT TGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGATCTG 806 CTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTTCCAATCAACAGAC 926 ATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGAT TGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTT 1046 GTAATGCCATCTTCACAGGTAAGAAATGCTCACAACAATGTGTAACGGCTGGGATGAGG 12; Gaps Length 1230025; Indels Score 208.2; DB 4; Pred. No. 4.5e-54; 0; Mismatches 413; or g or ö 1207936 ATGCTGAAATGAT 1207924 17.5%; NAME/KEY: misc feature LOCATION: (900001)...(915000) OTHER INFORMATION: n=a or c NAME/KEY: misc\_feature 1106 ATAAAGCCATGTT 1118 Query Match Best Local Similarity 53.5' Matches 488, Conservative 746 326 206 999 989 998 986 원 셤 ઠે ò ઠે ò a g ò ò 셤 ઠે 셤 ò g ò 셤 ò 셤 q ò ઠે 8 셤 ò ð ò

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1198075 AGCTTCTTCATGTTCTTGCAACAAGAGATCATATCCCAGAATCGGTACCTGTAAATTTAC 1198016
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APPLICANT: NISHIO, Shoichi
APPLICANT: AKIMARU, Jiro
APPLICANT: MITSUDA, Satoshi
ITILE OF INVENTION: DNA Fragments Containing Biotin Biosynthetase Gene and
ITILE OF INVENTION: Use of the Same
                                                                           1198015 TTTGGCCGATTGACGCCACGCCTTTGCAAGACCAGCCTCCGA-----TTTCTTTCT
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                                                                                                                                                                                                                                        926 ATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGAT
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llarity 52.4%; Pred. No. 5.7e-55;
Conservative 0; Mismatches 448; Indels 15;
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CURRENT APPLICATION NUMBER: US/09/180,109A
CURRENT FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 09/047838 JAPAN
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 1420
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US-09-180-109A-23
*, Sequence 23, Application US/09180109A
; Patent No. 6410293
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ORGANISH: Sphingomonas paucimobilis
FEATURE:
OTHER INFORMATION: Strain = JCM7511
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LOCATION: (223)..(1245)
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APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Malman, Sue
APPLICANT: Talman, Sue
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1998-11-12
PRIOR PILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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                                                                                                                      Sequence 1, Application US/09438185A
Patent No. 6822071
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; ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1
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Search completed: September 17, 2005, 20:39:10 Job time : 251 secs

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(without alignments)
8678.876 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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| cgn2 6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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| cgn2 6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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    5.1.6
Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli Sequence 6038, Ap Sequence 28355, A Sequence 180438, Sequence 29, Appl Sequence 29, Appl
\$ Query Match Length DB ID	10 US-09-722-957B-1 21 US-10-741-849-6038 10 US-10-425-114-28355 10 US-10-425-115-180438 9 US-09-740-2885-29 16 US-10-431-544-29 18 US-10-390-472-1
DB	10 12 18 18 20 9 U
å Query Match Length DB ID	1188 1125 1334 1345 1659 1659
% Query Match	100.0 35.2 32.5 32.5 29.4 27.6
Score	1188 417.6 386.2 386.2 349.2 328.2
Result No.	1264506

Sequence 18311, A	15	17.	e 17,	3, 2	۵	283	e 7	-	, ,		Sequence 579, App	e 579	9 1,	25,	ທ	11,	÷.	27, P	e 27,	7490	6.4	10	19,	e 19,	31,	e 31,	8411	a)	Sequence 7073, Ap	e 22203	Seguence 42017, A	Sequence 1, Appli	Ļ,	Sequence 1, Appli	145	Sequence 284, App
19 US-10-437-963-18311	3 03-03-740-286A-21 16 119-10-431-544-21	9 US-09-740-288A-17	6 US-10-43	9 US-09-740-288A-23	9	8 US-10-425-114-28	0 US-10-425-115-7	9 US-09-740-288A-7	9	9 US-10-767-701-13	9 US-09-938-842A-579	US-09-938-842A-5	21 US-10-702-364-1	US-09-740-288A-2	16 US-10-431-544-25	כ	3-10-43	₽		-7	US-10-424-599-2474	US-10-425-114-1	US-09-740-288A-1	16 US-10-431-544-19	9 US-09-740-288A-31	9	17 US-10-282-122A-8411	7 US-10-282-	ns-09-	US-10-282-122A-22	US-10-282-122A	17 US-10-329-670-1	US-10-158	2 US-10-98	2	17 US-10-312-273-284
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318.2		310.2				310.2	310.2	306.6	306.6	305.4	304	304	304	295.6	295.6	294.4	294.4	292.8	292.8	292.2	292.2	279.8	260.8	260.8	243.4	243.4			223.6	223.6		211.6	211.6	211.6	210.4	208.2
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## ALIGNMENTS

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Publication No. US20030104584A1

Publication No. US20030104584A1

ABPLICATION:
TITLE OF INVENTION:
FILE REFERENCE: C. utilis BIO2 - biotin synthase
CURRENT APPLICATION NUMBER: US/09/752,957B

CURRENT FILING DATE: 2003-01-10

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTAGGGCTACTCTGGCAACAGGTGCTACTGCTGCGGAGATCTTGGAAGATGTGTTC 120
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Best Local Similarity 100.
Matches 1188; Conservative
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Candida utilis
                                                                                                                                                                                                                                   LENGTH: 1188
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APPLICANT: Roemer, Terry
APPLICANT: Janey, Bo
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APPLICANT: Janey, Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of TITLE OF INVENTION: NUMBER: US/10/741,849
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.2
SEQ ID NO 6038
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Pred. No. 8.4e-116;
0; Mismatches 299;
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           Sequence 638, Application US/10741849
Publication No. US20050019931A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.2%;
Best Local Similarity 67.0%;
Matches 645; Conservative
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Candida albicans
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Excellic, David K.
APPLICANT: Excellic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 180438
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                                                                                                                          GCTATATATGACACCACTCATGGACTTGATGCACTATGCTCAGGTGCAACACAGAAGG 288
                                                                                                                                                                                                                  AGTGAAGACTGTTCCTACTGCGCCCAGTCATCTCGCTACGACACCGGTCTCAAAGCCACA 420
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 Pred. No. 3.4e-106;
0; Mismatches 353; Indels
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   63.0%;
                     617; Conservative
Best Local Similarity
Matches 617; Conserv
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APPLICANT: Kinney, Anthony
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US 60/172929
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR APPLICATION NUMBER: US 60/172929
SPRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 29 US/09740288A 29.4%; Query Match
Best Local Similarity 60.6
Matches 595; Conservative Sequence 29, Application U Patent No. US20010039042A1 , ORGANISM: Glycine max US-09-740-288A-29 GENERAL INFORMATION: 833 894 ò g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY SELF-ASSEMBLY OF AMPHIBHILLC PEPTIDES AND USES
                                                                                                                                                                                                714 ATGTGGATACGTCGAGGGATTTCTATCCCAAGGTTATCACGACCAGGGCTTATGATGAGA
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TCAAAGAGATGATCACTGCTGTCCATGACCTTGGAATGGAGAGTTGTGTCACCCTGGGAA
                                  rcadadeadricerraceagarrecegadaregeraregaderarerererere
                                                                                TGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATA
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
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APPLICATION NUMBER: US/10/390,472
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Lockshin, Curtis
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ADDRESSEE: HAMILTON, BROOF
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10390472; Publication No. US20040087013A1
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
Zhang, Shuguang
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US-10-390-472-1
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                                                                                                                                                                                                                                                                      TGCTCACAACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTC 1132
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                                                                                                                                    ATGAAGAAGTTAAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTG
                                                          AAGGA-----AACAAGAAGGTGGAATTTGAGAATATGTTGAGAATGGTTGCGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/10431544
Publication No. US20030192073A1
GENERAL INPORMATION:
APPLICANT: Allen, Steve
APPLICANT: Kinney, Tony
APPLICANT: Miao, Gou-Hua
APPLICANT: Miao, Gou-Hua
APPLICANT: Miao, Gou-Hua
APPLICANT: Miao, Gou-Hua
CINCENT:
CURRENT APPLICATION NUMBER: US/10/431,544
CURRENT APPLICATION NUMBER: 60/172929
PRIOR FILING DATE: 1999-12-21
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SOFTWARE: Microsoft Office 97
SEQ ID NO 29
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ORGANISM: Glycine max
US-10-431-544-29
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nes 595; Conserv
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APPLICANT: La Rosa, Thomas J.
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APPLICANT: Cao, Yongwei
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APPLICANT: Cao, Yongwei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Brad
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APPLICANT: Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCCAATCACAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCTTTCAATAAAGACAGGTGGGTGCAGCGAAGATTGTTCATACTGCCCCCAGTCCTCA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 GCAAAAAGGCAAAGGAGGCTGGGAGCACCCGCTTTTGCATGGGAGCAGCATGGAGAAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 ATGGGCATGGAGGTCTGTTGCACTCTTGGCATGCTAGAGAAGCAACAAGCTGAAGAACTC 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 AACACCTGGACCAAAGAAATTAAAGCTATATATGACACCACCACTCATGGACTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACAACCTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 TTCCACGGGGCTCAAGTCCATAGAAGTGTCCATAAATTCAGAGAAGTGCAACAGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 ACCATTGGGAGGAAAACAAATTTTAATCAGATCCTTGAATATGTCAAGGACATTAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 CTTGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 AAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCA
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Pred. No. 1.8e-85;
0; Mismatches 373; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_23882C.1
US-10-437-963-18311
                                                                                                                                                                                 Sequence 18311, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
606 GAGGCATTTAAGTACGA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.5%;
Matches 561; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1024 GTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACA 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 ATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATG 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCCTGAGTCCCTA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTATCCAAAGGTGATCTCCCACAAGAAGCTTTGATGATAGATTGAAAAACATTCAAAAAC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCAAGGATCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAA 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAATTAATAGACTAGTTGCTATCAAAGGGACTCCAATGGCTGAGGAACTTGCCGATCCA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAACAAGCAAGTTGAAGATTGACAGAACCATTGCTACTGCAAGATTGGTC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGCGAGAATAGTT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.6%; Score 328.2; DB 18; Length 72.1%; Pred. No. 2.5e-88; ive 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1292..2590
OTHER INFORMATION: /product='"zuotin"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284
FILING DATE: 22-AUG-1994
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGINT INFORMATION:
NAME: Brook, David E
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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Best Local Similarity 72.1'
Matches 445; Conservative
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Pred. No. 1.6e-83;
0; Mismatches 377;
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APPLICANT: Allen, Steve
APPLICANT: Miao, Gou-Hua
APPLICANT: Miao, Gou-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: 105/10/431,544
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: 60/172929
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; Sequence 21, Application US/10431544
; Publication No. US20030192073A1
; GENERAL INFORMATION:
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SOFTWARE: Microsoft Office 97
SEQ ID NO 21
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Matches 557; Conservative
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ORGANISM: Zea mays
US-10-431-544-21
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585 GCTGGAATAAGCATATGCTCAGGTGGAATTATTGGTCTTGGAGAGGCAGAGGAGGACCGT 744
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Sequence 21, Application US/0974028BA
Patent No. US2000039042A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Kinney, Anthony
APPLICANT: Maney, Anthony
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/09/740,28BA
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
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ORGANISM: Zea mays
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APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NB.
CURRENT APPLICATION NUMBER: US/09/740,288A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
                                                                                                                                                                          TYPE: DNA
ORGANISM: Hordeum vulgare
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                             AACGACTGGAGCCGGCCCGAGATCCAGCCGTCTACGACTCACCGCTCCTCGACCTCCTC
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RESULT 11 US-09-740-288A-17 ; Sequence 17, Application US/09740288A ; Patent No. US20010039042A1

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GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua

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APPLICANT: Kinney, Anthony
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/09/740, 288A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-21
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; Patent No. US20010039042A1
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SOFTWARE: Microsoft Office 97
SEQ ID NO 23
LENGTH: 1439
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; ORGANISM: Zea mays
US-09-740-288A-23
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59.0%; Pred. No. 4.8e-83;
ive 0; Mismatches 378; Indels
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APPLICANT: Kinney, Tony
APPLICANT: Kinney, Tony
APPLICANT: Miao, Gou-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US AN
CURRENT APPLICATION NUMBER: US/10/431,544
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEO ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 17, Application US/10431544; Publication No. US20030192073A1; GENERAL INFORMATION:
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US-10-431-544-17
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Local Similarity 59.0%; Fred. No. 4.8e-83;
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US-10-425-114-28968
Sequence 28968, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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                                                                                                                                            ATGAAAGGTAGAAAGTCAAACTTGAAGAAATCAAAGAGATGATCACTGCTGTCCATGAC
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Sequence 23, Application US/10431544

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Kinney, Tony
APPLICANT: Miao, Gou-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION WUMBER: US/10/431,544

CURRENT APPLICATION NUMBER: 00/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO 23

LENGTH: 1439
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: The OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28958
LENGTH: 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.1%; Score 310.2; DB 18; Length Best Local Similarity 59.0%; Pred. No. 4.9e-83; Matches 556; Conservative 0; Mismatches 378; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB4767-018-H9_FLI
US-10-425-114-28968
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays
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September 17, 2005, 15:54:19; Search time 4431 Seconds (without alignments) 10205.451 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                 OM nucleic - nucleic search, using sw model
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Title: Perfect score: Sequence:	US-09-752-957F-1 1188 1 atgtcgtttatattgactgcaggttgcattcggtgcttga 1188
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	34239544 seqs, 19032134700 residues
Total number of	Total number of hits satisfying chosen parameters: 68479088

	<u>د</u>
Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%

100% 45 summaries	·	
Maximum Match Listing first	EST:*  1. gb_est1:* 2. gb_est2:* 4. gb_st3:* 5. gb_est3:* 6. gb_est4:* 7. gb_est5:* 7. gb_est6:* 9. gb_gss1:*	1
	Database :	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	· Length	DB	ID	Description
~	333.4	28.1	696	. 6	CNSO6HEG	AL398894 T7 end of
2	330.4	27.8	985	σ	CNS06Z34	T3 end
m	297	25.0	1301	m	CNS0A9XF	0 Arabido
4	296.2	24.9	955	σ	CNS07350	N
'n	294.4	24.8	1306	m	CNS0A9QQ	m.
9	292	24.6	1412	ო	AX109523	AY109523 Zea mays
7	291	24.5	696	7	C0004857	CO004857 EST793192
80	290.8	24.5	876	7	C0084519	CO084519 GR Ea01D
0	270	22.7	872	7	CF822545	EST6
c 10	266	22.4	834	7	CF822544	4
c 11	262.4	22.1	829	7	CF721966	CF721966 CCAI517TF
c 12	252.4	21.2	862	,	CF719376	CF719376 CCAEF16TO
13	251.6	21.2	781	9	CD852378	CD852378 DH0ALL27Z
c 14	251.4	21.2	770	ß	BU063672	
15	250.2	21.1	671	9	CA781203	CA781203 017F07AF
c 16	248.6	20.9	780	7	CF680028	
c 17	242	20.4	729	Ŋ	BU059880	BU059880 Fqr-C 0 G
18	240.6	20.3	811	7	CF448691	CF448691 EST685036
13	239.4	20.2	865	7	CF682137	CF682137 CCAGC25TR
20	239.4	20.2	948	7	CF721975	CF721975 CCAI517TR
21	239.2	20.1	635	Ŋ	BU634775	BU634775 008D07 In
22	237.2	20.0	822	٢	CO147058	CO147058 EST822111
c 23	237	19.9	825	7	CF690143	CF690143 CCABZ41TF
24	234.4	19.7	721	Ŋ	BU064578	BU064578 Fgr_5_D19
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AZ931212 474.dhz63 AV923483 AV923483 CA669980 SCSGAD100 BUG62717 Fgr_2_C13 BUG62716 Fgr_2_C13 AL394500 T3 end of AV923288 AV923288 AV923288 AV923288 AV92328 AV92328 CCF682132 CCAGC25TF CC717806 GR_EDJIN.Y CC717806 GR_EDJIN.Y CN175752 BSTZ56852 BUG25073 QHF7113.Y CN145395 WOUND1_28 CA583129 ESTG8825 CO1360074 FTWM05243 CO1360074 FTWM05243 CO1360074 ETWM05243 CO1360074 ETWM05243 CO1360074 ETWM05243 CO1360074 ETWM05243 CC749199 ESTG85544	NTS	DNA linear GSS 30-NOV-2001 library ASOAA from strain CLIB 533 ic survey sequence. accharomycotina; Saccharomycetes;	S Soudiet,J.L., Aigle,M., Artiguenave,F., Blandin,G., S Soudiet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Sautin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weisenbach,J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies L FEBS Lett. 487 (1), 3-12 (2000)	la,S., Artiguenave,F., Wincker,P., авсоmycetous yeasts: 5. Im	S (bases 1 to 969)  S Genoscope.  G Genoscope.  Direct Submission  L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,  2 tue Gaston Cremieux, CP 5706, 91057 ERYX cedex, FRANCE. (E-mail: Beqrefégenoscope.cns.fr   Web: www.genoscope.cns.fr)  This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces gervazzii, Zygosaccharomyces rouxii, Saccharomyces Rluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarxowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of
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FEATURES

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Genoscope.

Direct Submission

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

segretégenoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces raciguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of
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/note="similar to Saccharomyces cerevisiae ORF YGR286c [
BIO2 ; biotin synthetase ]
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                                                                                                                                            Souciet, J.L., Aigle, M., Artiguenave, P., Blandin, G., Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogaropoulos, O., Potier, S., Saurin, W., Tekaia, P., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                  Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 985)
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/mol_type="genomic DNA"
/strain="CBS 6340"
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llarity 66.0%; Pred. No. 3.2e-82;
Conservative 1; Mismatches 252;
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/clone="AY0AA015C04"
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AL421814
AL421814.1 GI:12205009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ATACAACCATAACATTGATACCTCCAGAGAACATTACAGTAAAGTCATCACCACAGAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                              <2. .>658
/note="similar to Saccharomyces cerevisiae ORF YGR286c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 GACTCCAATGGCTGAGGAACTTGCCGACCCGGCAAGTAAGAAGTTGCAATTCGATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 CTTGAAGAAATCAAAGAGATGATCACTGCTGTCCATGACCTTGGAATGGAGAGTTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGAAGAGAATTGAGGAGATGATTTCRAAAGTGAACGACATGGGGCTGGAAACATGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             762 AGGTGGTATTCTTGGTCTGTGAGACCCAAGAGGACCGTGTATCTTTCCTCTACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 TGGTGGTATCTTAGGTCTAGGTGAAAGCGAAGATGACCACATTGGTTTCATTTACACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGCCAATGTATGAAGAAGTTAAGAAC-----AAGCAAGTTGAAGTTTGATGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 CTTAAGAACTATCGCCACAGCCAGAATTGTCATGCCTAAGGCGATCATAAGACTTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 TATTTTCACCGGTAAGAAATGCTTACAACTATGTGTAACGGTTGGGATGAAGACAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 AATGTTGGCTAAGTGGGGCTTGCAACCTATGGAAGCCTTCGAATA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches 177; Indels
                                                                                  organism="Saccharomyces bayanus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 333.4; DB 9
Pred. No. 4.4e-83;
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     extremity of this insert.
Location/Qualifiers
                                                                                                                                                          /variety="uvarum"
/db xref="taxon:4931"
/clone="ASOAA011H02"
/clone lib="ASOAA"
/note="end : T7"
                                                                                                      /mol_type="genomic DNA"
/strain="CLIB 533"
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71.0%;
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DEFINITION ACCESSION VERSION

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V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA. Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length
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                                                                                                                                                        http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACACCTGGACCAAAGAAATTAAAGCTATATATGACACACCCACTCATGGACTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACGATTGGAGTAGAGATGAATCAAGTCTGTTTATGATTCTCTCCTCTTGACCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCATGGAGCTCAGGTTCATAGACATGTTCATAACTTCAGGGAGGTACAACAATGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAAGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGGGATGGAAGTTTGCTGCACCTTAGGCATGATTGAGAACAACAAGCACTAGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>AAAAGTGCTGGGTTGACGGCGTACAACCATTGATACTTACAAGGAACACTATCCA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCTACTTGCAGTGAAAGGTACTCCTCTTGAAG-----ACCAGAAGCCAGTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGICATCACTACTAGAAGITATGACGATCGCCTTGAAACICTTAGCCATGITCGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                /organisme."Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/clone="GSLTFB57ZG05"
/tissue_type="Flowers and buds"
/plasmid="pcMVSPORT_6"
/plasmid="pcMVSPORT_6"
/gene="At2g43360"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 297; DB 3;
Pred. No. 1.1e-72;
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Best Local Simi
Matches 538;
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HTC; GSLT CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases to 1301)

Gastelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Menard, M., Cruaud, C., Quetler, F., Scarpelli, C., Schachter, V.,

Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFB57ZG05 of Flowers and buds of strain col-0 of Arabidopsis
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Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
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      GTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTACAACACTGGTGTCAAGGCTG
                                            AGAAGCTCGTATCCGTGGATGCGGTGCTCAAGGAGGCCGAGGAGGCCAAGCAGAACGGAT
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Direct Submission
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Arabidopsis thallana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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                 /clone="BAQAB016H11"
/clone lib="BAQAB0"
complement(<3. ->689)
/note="similar to Saccharomyces cerevisiae ORF YGR286c
BIO2 ; biotin synthetase }"
/evidence=not_experimental
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Direct Submission

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 BVRY cedex, FRANCE. (B-mail:
8 eqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Rluyverozzii, Zygosaccharomyces rouxii,
Saccharomyces hansenii, Kluyveromyces harmotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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clone BA0AB016H11 of library BA0AB from strain CLIB 210 of
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Kluyveromyces lactis
Kluyveromyces lactis
Eukaryota; Bacomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 955)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                      GITGAIGAGAITGICAGAACCAITGCIACTGCAAGAITGGICAIGCCAACGICTAITAIC
                                                                                                                                                                                                             GGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACAATGTGTAACGGCTGGGAT
                                                                                                                  AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT
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Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
Buchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kluyveromyces lactis, genomic survey sequence
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/mol_type="genomic DNA"
/strāin="CLIB 210"
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FEBS Lett. 487 (1), 66-70 (2000)
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Submitted (25-APR-2002) Maize Mapping Project, University of
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.isstate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.isstate.edu.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
       639 AAGAAGGCTGGCCTCACTGCTTATAACCACAATCTTGATACTTCAAGAGAGTACTACCCA
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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                                                                                                                                                                                                                                      Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Vaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weiseenbach, J. and Salanoubar, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of EACs in conjunction with the Maize Mapping Project"
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Coccidioides posadasii

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Corpygenales; mitosporic Onygenales; Coccidioides

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S Gardner,M.J. and Cole,G.T.

Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags

Unpublished (2003)

Contect: Gardner MJ

The Institute for Genomic Research

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Seq primer: M3 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="spherules"
/lab_host="E. coli DH10B, Tl phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA
0.4 to 2.3 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
Score 291; DB 7; Length 96
Pred. No. 5e-71;
0; Mismatches 315; Indels
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    . 969
    /organism="Coccidioides"
/mol_type="mRNA"
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872 bp mRNA linear EST 01-APR-2004
EST699927 Coccidioides posadasii saprobic phase cDNA library, 2 to
4 kb Coccidioides posadasii cDNA clone CIDAG50 5' end, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 TACAGCTTACAACCATAATCTCGATACTTCAAAAGAATATTATCCCAACATTATTACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     936 CAGAACCATIGCTACTGCAAGATIGGTCATGCCAACGICTATTATCAGATIGGCTGCAGG
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                                                                 Score 290.8; DB 7; Length Pred. No. 5.5e-71; 0; Mismatches 342; Indels
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E (Dases 1 to 87c)

Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Ming,R.A.

Global assembly of Cotton ESTs

Unpublished (2004)

Lontact: Rod A. Wing

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/ woll type="mRNA"

// strain="C735"
// darzef="Laxon:199306"
// darzef="Laxon:199306"
// dev stage="saprobic phase (mycelia)"
// dev stage="saprobic phase (mycelia)"
// dev stage="coli DH10B, TI phage resistant"
// lab host="E. coli DH10B, TI phage resistant"
// lab host="E. coli DH10B, TI phage resistant"
// lab host="E. coli DH10B, Ti phase cDNA
library, 2 to 4 kb"
// note="vector: pExpress 1; Site_1: Not I; Site_2: Eco RV;
// note="vector: pExpress 1; Site_1: Not I; Site_2: Eco RV;
// coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"
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EST69926 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAG50 3' end, mRNA
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bukaryota, Fungii Ascomycota, Pezizomycotina, Eurotiomycetes,
Onygenales, Fungii Ascomycota, Coccidioides.
1 (bases 1 to 834)
Sandner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
773 TIGGICITGGIGAGACCCAAGAGGACCGIGIAICTIICCICIACACCTIGGCCACAAIGG
                                                                                                                                                                                                                                                                                          763 iedectriadergaacageacreceaceeceregerrearacacaceeceecereec
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llarity 61.6%; Pred. No. 6.1e-64;
Conservative 0; Mismatches 270; Indels
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Other ESTS: EST69927
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, 1
Tel: 301 838 0208
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Location/Qualifiers
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                                                                                                  Coccidioides posadasii
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Onygenales, mitosporic Onygenales, Coccidioides

1 (bases 1 to 872)
S Gardner, M. J. and Cole, G. T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
Unpublished (2003)
Other Esrs: Esrse9926
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 919
Fax: 301 838 9028
Email: gardner@tigr.org
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lab_host="E. coli DH10B, T1 phage resistant"
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mol_type="mRNA"
etrain="C735"
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clone="CIDAG50"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: gardner@tigr.org
Seq primer: M13 Reverse.
                                               CF822545.1 GI:45928602
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/db_xref="taxon:40410"

/clone="CCALS17"

/clone lib="C-neoformans strain JEC21"

/note="Vector: pCMVSport6; Site_1: Not1_EcoRV; The full

length, normalized library was prepared from a variety of

conditions using RNA provided by Joseph Heitman and

Jennifer Lodge
                                                                                                                                                                                                                              tch 22.1%; al Similarity 60.6%; 453; Conservative
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Best Local S:
Matches 453
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Rockville, MD 20850, USA
Tel: 301-838-3543
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/mol_type="mRNA"
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Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales;
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JEC21 cDNA library
Unpublished (2003)
Other_ESTs: CCAI517TR
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CF721966.1 GI:41576125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 301-838-0208
Email: crypt@tigr.org
Seg primer: TF.
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953 CAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAG 1012
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Cryptococcus neoformans var. neoformans cDNA clone CCAEF16, mRNA sequence. CF719376
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Score 262.4; DB 7; Length
Pred. No. 6.4e-63;
0; Mismatches 286; Indels
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CD852378 11-JUL-2003 TH DD MRNA linear EST 11-JUL-2003 DHOALL27ZF09ZZM1 HaDevR5 Helianthus annuus CDNA clone HaDevR527F09,
                                                                                                                                                                                                                                                                                                                                                                                                      1099 GATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATGGAGATTTCAAATAC 1158
Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 CTCAGGTGCAACACAGAAGGTTCCAACAACTTCAGAGGTTCAATTGTGCACTCTTATGA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                           1039 GCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACAATGTGTAACGGCTGG
                                                                                                                                                                                    31 ATTCGTCTCGCGCTGGCCGACACGAATTCAGCGAGACCGAACAAGCCATGGCCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTCAAGTTCATAGACATGCTCAGAATTTTAGGGAGGTTCAGCAGTGTACGCTTCTGT
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Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

1 (bases 1 to 781)
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/clone="HabowR227F09"
/tissue_type="4 days after self-pollination embryo"
/clone_lib="HabowRs"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/mol_type="mRNA"
/cultivar="psc8"
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Genoplante
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/dc_one="CCARET6"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full
/note="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full
/note="rector: pcmvs.com" strain JEC21"
/note: pcmvs.com; strain JEC21"
/note
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                                                                                                                                                                                                                             Tremellaceae
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                                                                                  Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGAGGTTGTCACCTCACGATCATGATGATCGATTGAGCACCATTGCTGCCGTGCGA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cereircearrearceaceaerrrecaegareceeaecaecereaerrrreceere 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 AACACACTTGTCCCTATCCCTGGTACTCCCCTCGAAGGC-----AACGAGCCTGTC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      919 GAAGTIGAIGAGATIGICAGAACCAIIGCIACIGCAAGAIIGGICAIGCCAACGICIAIT 978
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|mol_type="mRNA"
|strain="JEC21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 862;
                                                                                                                                                                                       Bukaryota, Fungi, Basidiomycota, Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales;
                                                                                                                                                                                                                                                                                                                                                                        enriched,
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                                                                                                                        var. neoformans)
Cryptococcus neoformans var.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Ge
Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@figr.org
Seg primer: TF
                                                                                                                                                                                                                                                                                                                                                                End sequencing of clones fr
JEC21 cDNA library
Unpublished (2003)
Other ESTs: CCAEFIGTR
Contact: Brendan Loftus
               GI:41573535
                                                                                                                                                                                                                                                                                                 (bases 1 to 862)
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                                                                                                                                                                                                                                                                   Filobasidiella.
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Matches 43
                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
           VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                     554
                                                                                                                                                                                                                                                                                    756 GAGGGACATGCGCGGACGAGAACAGCCTCAAGAACATCAAGGCCCATGGTCGAGGGCGT 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACAATGTGTAACGG 1094
                                                                                                                                                                                                                                                                                                                           CCATGACCTTGGAATGGAGGTTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCAC 614
                                                                                                                                                                                                                                                                                                                                                                CAAGGGCATGGGAATGGAGGTCTGCGTAACGCTGGGCATGATCGACGCGGAGCAGGCCAA 637
                                                                                                                                                                                                                                                                                                                                                                                                     TGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                      636 GGAGCTCAAGGCGGCAGGACTCACGGCGTACAACCACAATGTTGATACTAGCCGAGAGTT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 CCGTGATGCTGGAATTAATGTCTGCTCTGGTGGAATTCTGGGTCTTGGTGAGAGCAGCGA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana Cress, Reptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 671)
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Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
                                    /mol_type="mRNA"
/Btrain="NRL1 31084"
/db xref="taxon:5518"
/clone_lib="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 TTACCCCAACGTCATCACGACGCGCAGCTACGACGGGGGCGACTGCAGACACTGAGTCATGT
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                                                                                                                                                                         Length 770;
                                                                                                                                                                       Score 251.4; DB 5; Length
Pred. No. 8.3e-60;
0; Mismatches 236; Indels
                       zeae"
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                       organism="Gibberella"
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62.7%;
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ACACTGGGGCAAGGAAGAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAAGG 448
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Fungal Genet. Biol. 38 (2), 187-197 (2003)
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                                                                                                                                                                                                                                                                                                                           CAGGCCTTACAGCTTACAATCATAACCTTGATACATCAAGAGAGTACTACCTAATATCA
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                                   ATACTGGAGTGAAAGCTCAAAAGCTCATGAACAAGGATGCTGTTCTTGAAGCTGCACAAA
                                                                         GTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGACCTTGGAA
                                                                                                                                                                                                                           TGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTG
                                                                                                                                                                                                                                                                TGGAGGTTTGTTGTACGTTGGGAATGATAGAAAAGCAGCAGCCTTTAGAACTCAAGAAAG
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.

1 (bases 1 to 770)
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1...671
| organism="Arabidopsis thaliana"
| organism="Arabidopsis thaliana"
| mol_type="mRNA"
| coctype="Columbia"
| db_xref="teaxon:3702"
| neer-organ: leaf; vector: pBluescript; Mixed cDNA
| library of Arabidopsis and E. cichoracearum infected leaf
| from three weeks old Arabidopsis plants. Plants were
| harvested 3 days after infection and mRNA oligo dT
| selected."
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Welinder, K.G. sequencing of Erysiphe cichoracearum infected Arabidopsis
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                                    plants

Unpublished (2002)
Contact: Karen G Wellinder
Contact: Karen G Wellinder
Institut for bioteknologi
Aalborg Universitet
Schngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: 445 98141808
Email: kgw@bio.auc.dk.
Location/Qualifiers

Location/Qualifiers
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